

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 07:02:52 : Search time 54 Seconds
(without alignments)
697.626 Million cell updates/sec

Title: US-09-857-841-3

Perfect score: 53

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Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 46 | 86.8 | 771 | 3 | US-08-875-233-5 |
| 2 | 46 | 86.8 | 772 | 3 | US-08-875-233-14 |
| 3 | 46 | 86.8 | 792 | 3 | US-08-875-233-3 |
| 4 | 45 | 84.9 | 130 | 1 | US-08-090-193-14 |
| 5 | 45 | 84.9 | 130 | 1 | US-08-488-031-14 |
| 6 | 45 | 84.9 | 130 | 2 | US-08-486-569-14 |
| 7 | 45 | 84.9 | 130 | 2 | US-08-488-027-14 |
| 8 | 45 | 84.9 | 130 | 2 | US-08-090-193-14 |
| 9 | 45 | 84.9 | 130 | 2 | US-08-482-653-14 |
| 10 | 45 | 84.9 | 130 | 2 | US-08-482-658-14 |
| 11 | 45 | 84.9 | 130 | 3 | US-08-470-349-14 |
| 12 | 45 | 84.9 | 130 | 3 | US-08-475-610-14 |
| 13 | 45 | 84.9 | 130 | 5 | PCT-US92-00277-14 |
| 14 | 45 | 84.9 | 130 | 5 | PCT-US92-00278-14 |
| 15 | 45 | 84.9 | 131 | 1 | US-08-090-193-11 |
| 16 | 45 | 84.9 | 131 | 1 | US-08-488-031-11 |
| 17 | 45 | 84.9 | 131 | 2 | US-08-486-569-11 |
| 18 | 45 | 84.9 | 131 | 2 | US-08-488-027-11 |
| 19 | 45 | 84.9 | 131 | 2 | US-08-090-193-11 |
| 20 | 45 | 84.9 | 131 | 2 | US-08-482-663-11 |
| 21 | 45 | 84.9 | 131 | 3 | US-08-482-658-11 |
| 22 | 45 | 84.9 | 131 | 3 | US-08-470-349-11 |
| 23 | 45 | 84.9 | 131 | 3 | US-08-475-610-11 |
| 24 | 45 | 84.9 | 131 | 5 | PCT-US92-00277-11 |
| 25 | 45 | 84.9 | 131 | 5 | PCT-US92-00278-11 |
| 26 | 45 | 84.9 | 152 | 1 | US-08-090-193-9 |
| 27 | 45 | 84.9 | 152 | 2 | US-08-488-031-9 |

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| 28 | 45 | 84.9 | 152 | 2 | US-08-486-569-9 | Sequence 9, Appl |
| 29 | 45 | 84.9 | 152 | 2 | US-08-488-027-9 | Sequence 9, Appl |
| 30 | 45 | 84.9 | 152 | 2 | US-08-090-192-9 | Sequence 9, Appl |
| 31 | 45 | 84.9 | 152 | 2 | US-08-482-663-9 | Sequence 9, Appl |
| 32 | 45 | 84.9 | 152 | 3 | US-08-482-658-9 | Sequence 9, Appl |
| 33 | 45 | 84.9 | 152 | 3 | US-08-470-349-9 | Sequence 9, Appl |
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| 35 | 45 | 84.9 | 152 | 5 | PCT-US92-00277-9 | Sequence 9, Appl |
| 36 | 45 | 84.9 | 154 | 1 | US-08-090-193-13 | Sequence 13, Appl |
| 37 | 45 | 84.9 | 154 | 2 | US-08-488-031-13 | Sequence 13, Appl |
| 38 | 45 | 84.9 | 154 | 2 | US-08-486-569-13 | Sequence 13, Appl |
| 39 | 45 | 84.9 | 154 | 2 | US-08-488-027-13 | Sequence 13, Appl |
| 40 | 45 | 84.9 | 154 | 2 | US-08-090-192-13 | Sequence 13, Appl |
| 41 | 45 | 84.9 | 154 | 2 | US-08-482-663-13 | Sequence 13, Appl |
| 42 | 45 | 84.9 | 154 | 3 | US-08-482-658-13 | Sequence 13, Appl |
| 43 | 45 | 84.9 | 154 | 3 | US-08-470-349-13 | Sequence 13, Appl |
| 44 | 45 | 84.9 | 154 | 3 | US-08-475-610-13 | Sequence 13, Appl |
| 45 | 45 | 84.9 | 154 | 5 | PCT-US92-00277-13 | Sequence 13, Appl |

ALIGNMENTS

RESULT 1
US-08-875-233-5
Sequence 5, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L.
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M.
APPLICANT: Reynolds, John F.
APPLICANT: Carney, Kim J.
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stearns, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60689
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber mosaic virus
STRAIN: V-34
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
OTHER INFORMATION: /codon_start=3
OTHER INFORMATION: /function="ENCAPSIDATES VIRUS RNA"

OTHER INFORMATION: /product= "COAT PROTEIN"
OTHER INFORMATION: /gene= "Cp"
OTHER INFORMATION: /number= 1
OTHER INFORMATION: /standard_name= "COAT PROTEIN"
US-08-875-233-5

Query Match 86.8%; Score 46; DB 3; Length 771;
Best Local Similarity 100.0%; Pred. No. 5.9e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 1 CCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46

RESULT 2

US-08-875-233-14
Sequence 14, Application US/08875233
Patent No. 6127601

GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L.
APPLICANT: Tricoll, David M.
APPLICANT: Reynolds, John F.
APPLICANT: Carney, Kim J.
TITLE OF INVENTION: Plants Resistant to C Strains of
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Steetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875.233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: A35
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
US-08-875-233-14

Query Match 86.8%; Score 46; DB 3; Length 772;
Best Local Similarity 100.0%; Pred. No. 5.9e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 1 CCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46

RESULT 3
US-08-875-233-3
Sequence 3, Application US/08875233
Patent No. 6127601

GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L.
APPLICANT: Tricoll, David M.
APPLICANT: Reynolds, John F.
APPLICANT: Carney, Kim J.
TITLE OF INVENTION: Plants Resistant to C Strains of
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Steetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875.233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: v-33
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
US-08-875-233-3

Query Match 86.8%; Score 46; DB 3; Length 792;
Best Local Similarity 100.0%; Pred. No. 5.9e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 1 CCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 46

RESULT 4

US-08-090-193-14
Sequence 14, Application US/08090193
Patent No. 5641673

GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5641673bert
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090,193
; FILING DATE: 23-DEC-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0609.3080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-090-193-14

Query Match 84.9%; Score 45; DB 1; Length 130;
Best Local Similarity 100.0%; Pred.No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 49
DB 52 CATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 96

RESULT 5
US-08-488-031-14
; Sequence 14, Application US/08488031
; Patent No. 5849548
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Peritmon, No. 5849548bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,031
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/090,193
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3080002/MAC/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2540
; TELEFAX: (202) 371-2600
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; US-08-488-031-14

Query Match 84.9%; Score 45; DB 2; Length 130;
Best Local Similarity 100.0%; Pred.No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 49
DB 52 CATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 96

RESULT 6
US-08-486-569-14
; Sequence 14, Application US/08486569
; Patent No. 5863774
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Peritmon, No. 5863774bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/090,193
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3080006/MAC/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
US-08-486-569-14

Query Match 84.9%; Score 45; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CATGACAAATCTGAATCAACCAAGTCTGTCGTAACCGTCGACG 49
Db 52 CATGACAAATCTGAATCAACCAAGTCTGTCGTAACCGTCGACG 96

RESULT 7

US-08-488-027-14
; Sequence 14, Application US/08488027
; Patent No. 5865384
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perrimon, No. 5866384bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,027
; FILING DATE: 07-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/090,193
; FILING DATE: 23-DEC-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3080003/MAC/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
US-08-488-027-14

Query Match 84.9%; Score 45; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 CATGACAAATCTGAATCAACCAAGTCTGTCGTAACCGTCGACG 49

Db 52 CATGACAAATCTGAATCAACCAAGTCTGTCGTAACCGTCGACG 96

RESULT 8
US-08-090-192-14
; Sequence 14, Application US/08090192
; Patent No. 5874414
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090,192
; FILING DATE: 11-NOV-1993
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/ US 92/00278
; FILING DATE: 16-JAN-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,333
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbal, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0609.3030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-090-192-14

Query Match 84.9%; Score 45; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CATGACAAATCTGAATCAACCAAGTCTGTCGTAACCGTCGACG 49
Db 52 CATGACAAATCTGAATCAACCAAGTCTGTCGTAACCGTCGACG 96

RESULT 9
US-08-482-663-14
; Sequence 14, Application US/08482663
; Patent No. 5882807
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perrimon, No. 5882907bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,663
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/090,193
 FILING DATE: 23-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/00277
 FILING DATE: 16-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/642,330
 FILING DATE: 17-JAN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Bugalsky, Lawrence B.
 REGISTRATION NUMBER: 35,086
 REFERENCE/DOCKET NUMBER: 0609.3080005/MAC/LBB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 130 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 US-08-482-663-14

Query Match 84.9%; Score 45; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.3e-15;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGATCAACCAAGTCTGCTGTAACCGTCGACG 49
 DB 52 CATGACAAATCTGATCAACCAAGTCTGCTGTAACCGTCGACG 96

RESULT 10
 US-08-482-658-14
 Sequence 14, Application US/08482658
 Patent No. 6010904
 GENERAL INFORMATION:
 APPLICANT: Haseloff, James
 APPLICANT: Brand, Andrea
 APPLICANT: Peritimon, No. 6010904bert
 APPLICANT: Goodman, Howard M.
 TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,658
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/090,193

FILING DATE: 23-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/00277
 FILING DATE: 16-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/642,330
 FILING DATE: 17-JAN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Bugalsky, Lawrence B.
 REGISTRATION NUMBER: 35,086
 REFERENCE/DOCKET NUMBER: 0609.3080008/MAC/LBB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 130 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 US-08-482-658-14

Query Match 84.9%; Score 45; DB 3; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.3e-15;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGATCAACCAAGTCTGCTGTAACCGTCGACG 49
 DB 52 CATGACAAATCTGATCAACCAAGTCTGCTGTAACCGTCGACG 96

RESULT 11
 US-08-470-349-14
 Sequence 14, Application US/08470349
 Patent No. 6015794
 GENERAL INFORMATION:
 APPLICANT: Haseloff, James
 APPLICANT: Goodman, Howard M.
 TITLE OF INVENTION: Trans-Splicing Ribozymes
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,349
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/090,192
 FILING DATE: 11-NOV-1993
 APPLICATION NUMBER: PCT/ US 92/00278
 FILING DATE: 16-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/642,333
 FILING DATE: 17-JAN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Cimbala, Michele A.
 REGISTRATION NUMBER: 33,851
 REFERENCE/DOCKET NUMBER: 0609.3030001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:

LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-470-349-14

Query Match 84.9%; Score 45; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTCTGTCTGTACCGTCGACG 49
DB 52 CATGACAAATCTGAATCAACCAAGTCTGTCTGTACCGTCGACG 96

RESULT 12
US-08-475-610-14
Sequence 14, Application US/08475610
Patent No. 6071730
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Peritmon, No. 6071730bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,610
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080004/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-475-610-14

Query Match 84.9%; Score 45; DB 3; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTCTGTCTGTACCGTCGACG 49
DB 52 CATGACAAATCTGAATCAACCAAGTCTGTCTGTACCGTCGACG 96

RESULT 13
PCT-US92-00277-14
Sequence 14, Application PC/TUS9200277
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
APPLICANT: Peritmon, Norbert
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 19920116
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3496604
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)833-7533
TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US92-00277-14

Query Match 84.9%; Score 45; DB 5; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTCTGTCTGTACCGTCGACG 49
DB 52 CATGACAAATCTGAATCAACCAAGTCTGTCTGTACCGTCGACG 96

RESULT 14
PCT-US92-00278-14
Sequence 14, Application PC/TUS9200278
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00278
FILING DATE: 19920116
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,333
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.34/6604
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 833-7533
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Nucleic Acid
PCT-US92-00278-14

Query Match 84.9%; Score 45; DB 5; Length 130;
Best Local Similarity 100.0%; Pred. No. 2,3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTCTGTCGTAAACCGTCGACG 49
DB 52 CATGACAAATCTGAATCAACCAAGTCTGTCGTAAACCGTCGACG 96

RESULT 15

US-08-090-193-11
Sequence 11, Application US/08090193
Patent No. 5641673
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Pettimon, No. 5641673bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,193
FILING DATE: 23-DEC-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-090-193-11

Query Match 84.9%; Score 45; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 2,3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CATGACAAATCTGAATCAACCAAGTCTGTCGTAAACCGTCGACG 49
DB 53 CATGACAAATCTGAATCAACCAAGTCTGTCGTAAACCGTCGACG 97

Search completed: December 5, 2004, 08:00:07
Job time : 54 secs

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OM protein - protein search, using sw model

Run on: December 5, 2004, 08:05:27 : Search time 71 Seconds
(without alignments)
70.735 Million cell updates/sec

Title: US-09-857-841-4

Sequence: 1 MDKSESTSGAGNR 14

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 14 | 100.0 | 14 | 3 | AAV90255 Ubiquitin |
| 2 | 14 | 100.0 | 218 | 2 | AAV10652 Capid pr |
| 3 | 14 | 100.0 | 218 | 2 | AAV10653 Capid pr |
| 4 | 14 | 100.0 | 218 | 2 | AAV57968 Cauliflow |
| 5 | 14 | 100.0 | 218 | 2 | AAV67753 CMV coat |
| 6 | 14 | 100.0 | 218 | 2 | AAV93803 Coat prot |
| 7 | 14 | 100.0 | 218 | 2 | AAV98893 Coat prot |
| 8 | 14 | 100.0 | 218 | 2 | AAV98894 Coat prot |
| 9 | 14 | 100.0 | 218 | 2 | AAV98895 Coat prot |
| 10 | 12 | 85.7 | 218 | 2 | AAV88053 Agrobacte |
| 11 | 11 | 50.0 | 70 | 4 | AAU40661 Propionib |
| 12 | 11 | 50.0 | 70 | 4 | AAU67189 Propionib |
| 13 | 11 | 50.0 | 70 | 6 | ABW63708 Propionib |
| 14 | 11 | 50.0 | 70 | 6 | ABW63708 Propionib |
| 15 | 11 | 50.0 | 107 | 3 | AAV21510 Arabidops |
| 16 | 11 | 50.0 | 147 | 3 | AAV21509 Arabidops |
| 17 | 11 | 50.0 | 147 | 8 | ADN73301 Thale cre |
| 18 | 11 | 50.0 | 175 | 3 | AAV21508 Arabidops |
| 19 | 6 | 42.9 | 15 | 4 | AAV86674 Human cyt |
| 20 | 6 | 42.9 | 15 | 4 | AAV86675 Human cyt |
| 21 | 6 | 42.9 | 15 | 4 | AAV86676 Human cyt |
| 22 | 6 | 42.9 | 15 | 7 | ADJ34279 MHC/HLA P |
| 23 | 6 | 42.9 | 15 | 7 | ADJ34282 MHC/HLA P |
| 24 | 6 | 42.9 | 15 | 7 | ADJ34285 MHC/HLA P |
| 25 | 6 | 42.9 | 15 | 7 | ADJ34281 MHC/HLA P |

| | | | | | |
|----|---|------|-----|---|--------------------|
| 26 | 6 | 42.9 | 15 | 7 | ADJ34276 MHC/HLA P |
| 27 | 6 | 42.9 | 15 | 7 | ADJ34280 MHC/HLA P |
| 28 | 6 | 42.9 | 15 | 7 | ADJ34283 MHC/HLA P |
| 29 | 6 | 42.9 | 15 | 7 | ADJ34278 MHC/HLA P |
| 30 | 6 | 42.9 | 15 | 7 | ADJ34284 MHC/HLA P |
| 31 | 6 | 42.9 | 15 | 7 | ADJ34277 MHC/HLA P |
| 32 | 6 | 42.9 | 20 | 6 | ABJ38036 Human cyt |
| 33 | 6 | 42.9 | 23 | 5 | AAE13475 Peptide # |
| 34 | 6 | 42.9 | 62 | 4 | AAU52188 Propionib |
| 35 | 6 | 42.9 | 62 | 6 | ABM48707 Propionib |
| 36 | 6 | 42.9 | 80 | 4 | AAV91216 Human imm |
| 37 | 6 | 42.9 | 82 | 7 | ABO74002 Pseudomon |
| 38 | 6 | 42.9 | 116 | 3 | AAV03795 Human sec |
| 39 | 6 | 42.9 | 118 | 2 | AAV72060 HSV-2 str |
| 40 | 6 | 42.9 | 146 | 7 | ABO75957 Pseudomon |
| 41 | 6 | 42.9 | 158 | 4 | AAV92693 Human dig |
| 42 | 6 | 42.9 | 180 | 4 | AAU65750 Propionib |
| 43 | 6 | 42.9 | 180 | 6 | ABM62269 Propionib |
| 44 | 6 | 42.9 | 196 | 3 | AAV32144 Human sec |
| 45 | 6 | 42.9 | 203 | 7 | ABO73932 Pseudomon |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | |
| AAV90255 | AAV90255 standard; protein; 14 AA. |
| XX | |
| AC | AAV90255; |
| DT | 19-SEP-2000 (first entry) |
| XX | |
| DE | Ubiquitin monomer C-terminal fragment. |
| XX | |
| KW | Ubiquitin monomer; protein production; plant cell; ubiquitin promoter. |
| XX | |
| OS | Nicotiana tabacum. |
| XX | |
| PN | MO200036129-A1. |
| PD | 22-JUN-2000. |
| XX | |
| PE | 11-DEC-1998; 98WO-SG000103. |
| XX | |
| PR | 11-DEC-1998; 98WO-SG000103. |
| XX | |
| PA | (MOLE-) INST MOLECULAR AGROBIOLOGY. |
| XX | |
| PI | Fang R, Wu J, Chen X; |
| XX | |
| DR | WPI; 2000-431604/37. |
| XX | |
| DR | N-PSDB; AAA30858. |
| XX | |
| PT | Production of desired protein in plants or plant cells by linking a |
| PT | ubiquitin monomer coding sequence upstream of the gene encoding the |
| PT | desired protein. |
| XX | |
| PS | Claim 7; Page 18; 42pp; English. |
| XX | |
| CC | This sequence represents the C-terminal fragment of a ubiquitin monomer. |
| CC | The invention relates to a method for enhancing production of a desired |
| CC | protein in a plant or plant cell by inserting a nucleic acid (NA) |
| CC | encoding a ubiquitin monomer upstream of a NA encoding the desired |
| CC | protein, where the fusion construct encodes a fusion protein and |
| CC | expression is not controlled by the ubiquitin promoter. The invention |
| CC | also relates to a NA acid vector a NA vector able to transform a plant |
| CC | cell, that comprises NA encoding a fusion protein having a ubiquitin |
| CC | monomer linked to a protein of interest and further, where expression of |
| CC | the fusion construct is not under control of a ubiquitin promoter. The |
| CC | construct allows enhanced production of the desired protein in plants or |
| CC | plant cells |

Sequence 14 AA;
Query Match 100.0%; Score 14; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKSESTSGRNR 14
1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14

RESULT 2
AAR10652
ID AAR10652 standard; protein; 218 AA.
XX
XX AAR10652;
AC
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-APR-1991 (first entry)
XX
XX Capsid protein of Cucumber Mosaic Virus strain FNY.
DE
XX CMV; resistance; capsid protein; Cucumis melo.
KM
XX Cucumber mosaic virus.
OS
XX EP412912-A.
PN 13-FEB-1991.
XX
XX 09-AUG-1990; 90EP-00402282.
PF
XX 11-AUG-1989; 89FR-00010848.
PR
XX (BIOC-) BIOCEM SA.
PA
XX Deboth M, Bentahar S, Noel M, Perret J;
PI WPI; 1991-046027/07.
XX N-PSDB; AAQ10461.
DR
XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
PT culture on specific medium for new transformed plants etc., esp.
PT resistant to cucumber mosaic virus.
PT
XX
XX Claim 15; Page 17; 44pp; French.
PS
XX The gene encoding this protein was isolated from a plasmid (pUC18)
CC containing DNA complementary to RNA 3 of the virulent strain FNY,
CC isolated in New York on infected melons. Transgenic melon plantlets
CC containing the nucleotide sequence introduced via an Agrobacterium
CC tumefaciens intermediate are cultured as shoots in special media. The
CC transformed melon plants are resistant to CMV. See also AAQ10462.
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
CC correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 218 AA;
SQ

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKSESTSGRNR 14
1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14

RESULT 3
AAR10653
ID AAR10653 standard; protein; 218 AA.
XX
XX AAR10653;
AC

XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-APR-1991 (first entry)
XX
XX Capsid protein of Cucumber Mosaic Virus strain 117F.
DE
XX CMV; strain 117F; resistance; capsid protein; Cucumis melo.
KM
XX Cucumber mosaic virus.
OS
XX EP412912-A.
PN 13-FEB-1991.
XX
XX 09-AUG-1990; 90EP-00402282.
PF
XX 11-AUG-1989; 89FR-00010848.
PR
XX (BIOC-) BIOCEM SA.
PA
XX Deboth M, Bentahar S, Noel M, Perret J;
PI WPI; 1991-046027/07.
XX N-PSDB; AAQ10462.
DR
XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
PT culture on specific medium for new transformed plants etc., esp.
PT resistant to cucumber mosaic virus.
PT
XX
XX Claim 16; Page 19; 44pp; French.
PS
XX The gene encoding this protein was isolated from the virulent French
CC strain 117F of CMV. Transgenic melon plantlets containing the coding
CC sequence (introduced via an Agrobacterium tumefaciens intermediate) are
CC cultured as shoots in special media. The transformed melon plants are
CC resistant to CMV. See also AAQ10461. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
CC AUG-2003 to correct OS field.)
XX
XX Sequence 218 AA;
SQ

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKSESTSGRNR 14
1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14

RESULT 4
AAR57968
ID AAR57968 standard; protein; 218 AA.
XX
XX AAR57968;
AC
XX 25-MAR-2003 (revised)
DT 20-APR-1995 (first entry)
XX
XX Cauliflower mosaic virus capsid protein.
DE
XX Cauliflower mosaic virus; CMV; capsid protein; coat protein;
KW polyribosyme; inactivate; inactivation; resistance; crop protection.
XX Cauliflower mosaic virus.
OS
XX FR2701960-A1.
PN
XX 02-SEP-1994.
PD
XX 26-FEB-1993; 93FR-00002269.
PF
XX

PR 26-FEB-1993; 93FR-00002269.
XX (GENE-) GENE SHEARS PTY LTD.
XX
PI Lenee P, Perez P, Gruber V, Baudot G, Ollivo C;
XX WPI; 1994-281767/35.
DR N-PSDB; AA067395.
XX
PT New polyribozyme contg. several catalytic regions in complementary
PT sequence - can inactivate gene for viral capsid protein, esp. for prepn.
PT of new virus resistant transgenic plants, also DNA sequence encoding it.
XX
PS Disclosure; Fig 2; 67pp; French.
XX The RNA encoding the capsid protein of cauliflower mosaic virus can be
XX targeted by a nucleic acid sequence called a "polyribozyme". The
XX polyribozyme has endoribonuclease activity and is able to inactivate the
XX gene encoding the viral capsid protein. The polyribozyme comprises
XX several catalytic regions derived from ribozymes and confers complete
XX resistance to virus. See AA067391-94. (Updated on 25-MAR-2003 to correct
XX PN field.)
XX
SQ Sequence 218 AA;
XX
Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-06; Mismatches 0; Gaps 0;
Matches 14; Conservative 0; Indels 0;
OY 1 MDKSESTSGRRNR 14
DB 1 MDKSESTSGRRNR 14
XX
RESULT 5
AAR67753 standard; protein; 218 AA.
XX
AC AAR67753;
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE CMV coat protein.
XX
KW Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; coat protein; CP;
KW TMV; CMV.
XX
OS Cucumber mosaic virus.
XX
PN WO9429464-A1.
XX
XX 22-DEC-1994.
XX
PF 03-JUN-1994; 94WO-EP001817.
XX
PR 04-JUN-1993; 93GB-00011593.
XX
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERM GBS MBH.
XX
PI De Haan PT;
XX
DR WPI; 1995-036490/05.
DR N-PSDB; AA076106.
XX
PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.

XX
PS Disclosure; Page 30; 50pp; English.
XX
CC A chimeric cucumber mosaic virus RNA-3 (given in AA076106) codes for the
CC coat protein (CP) of tomato mosaic virus (AAR67552) as well as its own CP
CC (AAR67753). The construct elicits minus-sense RNA that interacts with the
CC RNA-dependent RNA-polymerase of an invading virus, thus conferring virus-
CC resistance on a host plant, e.g. tobacco, tomato. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 218 AA;
XX
Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-06; Mismatches 0; Gaps 0;
Matches 14; Conservative 0; Indels 0;
OY 1 MDKSESTSGRRNR 14
DB 1 MDKSESTSGRRNR 14
XX
RESULT 6
AAR93803 standard; protein; 218 AA.
XX
AC AAR93803;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the A35 strain of cucumber mosaic virus.
XX
KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KW resistance.
XX
OS Cucumber mosaic virus; strain A35.
XX
PN WO9621018-A1
XX
PD 11-JUL-1996.
XX
PF 07-JUN-1995; 95WO-US007234.
XX
PR 30-DEC-1994; 94US-00367789.
XX
PA (ASGR-) ASGROW SEED CO.
XX
PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
DR WPI; 1996-333993/33.
DR N-PSDB; AA17259.
XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
PS Disclosure; Fig 8; 80pp; English.
XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC squash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 218 AA;
XX
Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-06; Mismatches 0; Gaps 0;
Matches 14; Conservative 0; Indels 0;
OY 1 MDKSESTSGRRNR 14

| Db | 1 | MDKSESTSGARNRR | 14 |
|-----------------------|---|----------------------------|-------------|
| RESULT 7 | | | |
| ID | AAR98893 | standard; protein; 218 AA. | |
| XX | | | |
| AC | AAR98893; | | |
| XX | | | |
| DT | 16-OCT-2003 | (revised) | |
| DT | 02-DEC-1996 | (first entry) | |
| XX | | | |
| DE | Coat protein of the V27 strain of cucumber mosaic virus. | | |
| XX | | | |
| KW | Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35; resistance. | | |
| XX | | | |
| OS | Cucumber mosaic virus; strain V27. | | |
| XX | | | |
| PN | MO9621018-A1. | | |
| PD | 11-JUL-1996. | | |
| XX | | | |
| PP | 07-JUN-1995; | 95WO-US007234. | |
| XX | | | |
| PR | 30-DEC-1994; | 94US-00367789. | |
| XX | | | |
| PA | (ASGR-) ASGROW SEED CO. | | |
| XX | | | |
| PI | Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ; | | |
| XX | | | |
| DR | WPI; 1996-333993/33. | | |
| XX | | | |
| DR | N-PSDB; AAT34664. | | |
| XX | | | |
| PT | New isolated cucumber mosaic virus coat protein DNA - used to produce | | |
| PT | plants, partic. of the family Cucurbitaceae or Solanaceae, which are | | |
| PT | resistant to infection. | | |
| XX | | | |
| PS | Disclosure; Fig 1; 80pp; English. | | |
| XX | | | |
| CC | Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber | | |
| CC | mosaic virus (CMV) were isolated. The CMV CP genes were isolated from | | |
| CC | infected plant tissue by PCR amplification of cDNA using primers based on | | |
| CC | known CP sequences. The genes may be used for producing plants such as | | |
| CC | quash, cucumber, peppers and tomatoes which are resistant to CMV | | |
| CC | infection. (Updated on 16-OCT-2003 to standardise OS field) | | |
| XX | | | |
| SQ | Sequence 218 AA; | | |
| Query Match | 100.0%; | Score 14; | DB 2; |
| Best Local Similarity | 100.0%; | Pred. NO. 1.7e-06; | Length 218; |
| Matches 14; | Conservative 0; | Mismatches 0; | Indels 0; |
| Gaps 0; | | | |
| QY | 1 | MDKSESTSGARNRR | 14 |
| DB | 1 | MDKSESTSGARNRR | 14 |
| RESULT 8 | | | |
| ID | AAR98894 | standard; protein; 218 AA. | |
| XX | | | |
| AC | AAR98894; | | |
| XX | | | |
| DT | 16-OCT-2003 | (revised) | |
| DT | 02-DEC-1996 | (first entry) | |
| XX | | | |
| DE | Coat protein of the V33 strain of cucumber mosaic virus. | | |
| XX | | | |
| KW | Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35; resistance. | | |
| XX | | | |
| OS | Cucumber mosaic virus; strain V33. | | |

```

XX XX WO9621018-A1.
XX XX
XX PD 11-JUL-1996.
XX PF 07-JUN-1995; 95WO-US007234.
XX XX
XX PR 30-DEC-1994; 94US-00367789.
XX XX
XX PA (ASGR-) ASGROW SEED CO.
XX XX
XX PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX XX
XX DR WPI; 1996-333993/33.
XX DR N-PSDB; AAT34665.
XX XX
XX PT New isolated cucumber mosaic virus coat protein DNA - used to produce
XX PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
XX XX resistant to infection.
XX XX
XX PS Disclosure; Fig 2; 80pp; English.
XX XX
XX CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
XX CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
XX CC infected plant tissue by PCR amplification of cDNA using primers based on
XX CC known CP sequences. The genes may be used for producing plants such as
XX CC quash, cucumber, peppers and tomatoes which are resistant to CMV
XX CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX XX
XX SQ Sequence 218 AA;

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. NO. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MDKSESTSGAGNRR 14
DB 1 MDKSESTSGAGNRR 14

RESULT 9
AAR98895
ID AAR98895 standard; protein; 218 AA.
AC
XX AAR98895;
XX XX
XX DT 16-OCT-2003 (revised)
XX DT 02-DEC-1996 (first entry)
XX XX
XX DE Coat protein of the V34 strain of cucumber mosaic virus.
XX KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
XX KW resistance.
XX XX
XX CS Cucumber mosaic virus; strain V34.
XX XX
XX PN WO9621018-A1.
XX PD
XX PF 11-JUL-1996.
XX PF 07-JUN-1995; 95WO-US007234.
XX PR 30-DEC-1994; 94US-00367789.
XX XX
XX PA (ASGR-) ASGROW SEED CO.
XX XX
XX PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX XX
XX DR WPI; 1996-333993/33.
XX DR N-PSDB; AAT34666.
XX XX
XX PT New isolated cucumber mosaic virus coat protein DNA - used to produce
XX PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are

```


PT resistant to infection.
XX
XX
PS Disclosure; Fig 3; 80pp; English.
XX
XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
XX
SQ Sequence 218 AA;
Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MDKSESTAGRRNR 14
|||||
1 MDKSESTAGRRNR 14
DB
RESULT 10
ABR80503
ID ABR80503 standard; protein; 218 AA.
XX
XX ABR80503;
XX
XX 25-JUL-2002 (first entry)
XX
XX Agrobacterium tumefaciens protein sequence.
XX
XX Agrobacterium tumefaciens; anti-cucumber mosaic virus; transgenic tomato.
XX
XX Agrobacterium tumefaciens.
XX
XX KR99075101-A.
XX
XX 05-OCT-1999.
XX
XX 17-MAR-1998; 98KR-00009096.
XX
XX 17-MAR-1998; 98KR-00009096.
XX
XX (RURA-) RURAL DEV ADMINISTRATION.
XX
XX Sohn SH, Lee SW, Park JS, Hwang YS;
XX
XX WPI; 2000-577926/54.
XX
XX N-PSDB; ABL58209.
XX
XX Anti-cucumber mosaic virus tomato.
XX
XX Disclosure; Page 4; 6pp; Korean.
XX
XX
CC This sequence represents a protein sequence from Agrobacterium
CC tumefaciens used within the scope of the invention. The invention relates
CC to an anti-cucumber mosaic virus tomato
XX
XX
SQ Sequence 218 AA;
Query Match 85.7%; Score 12; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
3 KSESTAGRRNR 14
|||||
3 KSESTAGRRNR 14
DB
RESULT 11
AAU40661
ID AAU40661 standard; protein; 70 AA.

XX
XX AAU40661;
AC
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX Propionibacterium acnes immunogenic protein #1557.
DE
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant.
XX
XX
XX Propionibacterium acnes.
OS
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX
XX 02-JUN-2000; 2000US-0208841P.
XX
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
XX
XX N-PSDB; AAS59512.
XX
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
PT
XX
XX Example 1; SEQ ID NO 1856; 1069pp; English.
XX
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 70 AA;
Query Match 50.0%; Score 7; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
8 SAGRRNR 14
|||||
52 SAGRRNR 58
DB
RESULT 12
AAU67189
ID AAU67189 standard; protein; 70 AA.

XX AAU67189;
XX 27-FEB-2002 (first entry)
XX Propionibacterium acnes immunogenic protein #28085.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
XX
XX WO200181581-A2;
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX 02-JUN-2000; 2000US-0208841P.
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skelky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX MPI; 2001-616774/71.
XX N-PSDB; AAS59784.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX vaccinating against and diagnosing infections, especially useful for
XX treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 28384; 1069pp; English.
XX
XX Sequences AAU93105-AAU68017 represent Propionibacterium acnes immunogenic
XX polypeptides. The proteins and their associated DNA sequences are used in
XX the treatment, prevention and diagnosis of medical conditions caused by
XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX P. acnes is also involved in infections of bone, joints and the central
XX nervous system, however it is particularly involved in the inflammatory
XX lesions associated with acne vulgaris. A method for detecting the
XX presence or absence of P. acnes in a patient comprises contacting a
XX sample with a binding agent that binds to the proteins of the invention
XX and determining the amount of bound protein in the sample. The
XX polypeptides may be used as antigens in the production of antibodies
XX specific for P. acnes proteins. These antibodies can be used to
XX downregulate expression and activity of P. acnes polypeptides and
XX therefore treat P. acnes infections. The antibodies may also be used as
XX diagnostic agents for determining P. acnes presence, for example, by
XX enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 70 AA;
XX
XX Query Match 50.0%; Score 7; DB 4; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 8.3;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ABM63708;
XX 20-OCT-2003 (first entry)
XX Propionibacterium acnes predicted ORF-encoded polypeptide #28384.
XX
XX Acne vulgaris; anti-seborrheic; dermatological; antibacterial;
XX immunostimulant; immune response; vaccine.
XX
XX Propionibacterium acnes.
XX
XX WO2003033515-A1.
XX
XX 24-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032727.
XX
XX 15-OCT-2001; 2001US-00978825.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, Skelky YAM, Persing DH, Bhatia A, Maisonneuve JL;
XX Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
XX Barth B, Vallee-Douglas J;
XX MPI; 2003-381789/36.
XX N-PSDB; ACF64713.
XX
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
XX polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX or for stimulating an immune response specific for a P. acnes protein.
XX
XX Example 1; SEQ ID NO 28384; 1481pp; English.
XX
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
XX encoding a Propionibacterium acnes protein. The invention also relates to
XX polypeptides encoded by the polynucleotides (ABM55624-ABM64536) and to
XX immunogenic fragments of P. acnes polypeptides. The invention
XX additionally encompasses expression vectors and host cells comprising a
XX polynucleotide of the invention; antibodies against polypeptides of the
XX invention; fusion proteins comprising a polypeptide of the invention; a
XX method for stimulating an immune response specific for a P. acnes
XX polypeptide and an isolated T cell population comprising T cells prepared
XX via this method; a vaccine composition (comprising P. acnes polypeptides,
XX polynucleotides, antibodies, fusion proteins, T cell populations, or
XX antigen-presenting cells that express the polypeptide); a method and kit
XX for detecting or determining the presence or absence of P. acnes in a
XX patient; and a method for inhibiting the development of P. acnes in a
XX patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
XX proteins, T cell populations or antigen-presenting cells that express the
XX polypeptides are useful for diagnosing, preventing or treating acne
XX vulgaris, or for stimulating an immune response specific for a P. acnes
XX protein. The polynucleotides can also be used as probes or primers for
XX nucleic acid hybridisation. The vaccine composition is useful for the
XX stimulation of an immune response against P. acnes, or for treating acne,
XX and the kit is useful for performing a diagnostic assay. The present
XX sequence represents a polypeptide predicted to be encoded by an ORF (open
XX reading frame) contained within the P. acnes polynucleotides of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 70 AA;
XX
XX Query Match 50.0%; Score 7; DB 6; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 8.3;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
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PR 06-JUL-1999; 99US-0142390P.
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PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 10-AUG-1999; 99US-0147935P.
PR 11-AUG-1999; 99US-0148171P.
PR 12-AUG-1999; 99US-0148319P.
PR 13-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.

PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149446P.
PR 20-AUG-1999; 99US-0149722P.
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
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PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
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PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
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PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
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PR 21-OCT-1999; 99US-0160768P.
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PR 22-OCT-1999; 99US-0160980P.
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PR 25-OCT-1999; 99US-0161404P.
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PR 26-OCT-1999; 99US-0161350P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 50.0%; Score 7; DB 3; Length 107;
Best Local Similarity 100.0%; Pred.No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KSESTSA 9
|||
Db 96 KSESTSA 102

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 06:39:02 ; Search time 1482 Seconds
(without alignments)
1303.175 Million cell updates/sec

28
104
#6

Title: US-09-857-841-3

Perfect score: 53

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Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 1821985908 residues

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Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gsa1:
9: gb_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| C 1 | 45 | 84.9 | 127 | 4 | BM067231 KS08001E1 |
| C 2 | 20 | 37.7 | 287 | 2 | BB440162 BB440162 |
| C 3 | 18 | 34.0 | 288 | 2 | BB006007 BB006007 |
| C 4 | 18 | 34.0 | 316 | 2 | BB494132 BB494132 |
| C 5 | 18 | 34.0 | 428 | 6 | CA016832 HV05N02u |
| C 6 | 18 | 34.0 | 500 | 6 | CA017649 HV05N02r |
| C 7 | 18 | 34.0 | 597 | 5 | BO585418 E012691-0 |
| C 8 | 18 | 34.0 | 608 | 4 | BM333093 MEST183-H |
| C 9 | 18 | 34.0 | 611 | 4 | BM347598 MEST279-G |
| C 10 | 18 | 34.0 | 627 | 9 | AG223668 Lotus cor |
| C 11 | 18 | 34.0 | 629 | 4 | BI271889 NF014E05F |
| C 12 | 18 | 34.0 | 688 | 5 | BM752014 BX752014 |
| C 13 | 18 | 34.0 | 688 | 7 | CK185060 EST774375 |
| C 14 | 18 | 34.0 | 701 | 6 | CB634510 OS11B14B |
| C 15 | 18 | 34.0 | 713 | 6 | CC501966 CH240_340 |
| C 16 | 18 | 34.0 | 735 | 5 | CB618020 OS11Ea01J |
| C 17 | 18 | 34.0 | 742 | 5 | BM874992 BX874992 |
| C 18 | 18 | 34.0 | 760 | 6 | AG379970 Mus muscu |
| C 19 | 18 | 34.0 | 778 | 7 | CK180493 EST779808 |
| C 20 | 18 | 34.0 | 816 | 4 | CC708428 OSULP54TV |
| C 21 | 18 | 34.0 | 833 | 4 | BG299724 HVSMBa002 |
| C 22 | 18 | 34.0 | 877 | 6 | CB622656 OS11Ea09K |
| C 23 | 18 | 34.0 | 881 | 5 | BX749432 BX749432 |
| C 24 | 18 | 34.0 | 881 | 5 | BX749432 BX749432 |

date
104
#6

| | | | | | |
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| C 25 | 18 | 34.0 | 909 | 9 | CG281996 |
| C 26 | 18 | 34.0 | 915 | 2 | CG708421 |
| C 27 | 18 | 34.0 | 959 | 9 | BE421380 |
| C 28 | 18 | 34.0 | 971 | 9 | CG281990 |
| C 29 | 17 | 32.1 | 251 | 1 | AV246895 |
| C 30 | 17 | 32.1 | 268 | 2 | BB087806 |
| C 31 | 17 | 32.1 | 348 | 6 | CD483766 |
| C 32 | 17 | 32.1 | 494 | 7 | W31931 |
| C 33 | 17 | 32.1 | 584 | 8 | BH004925 |
| C 34 | 17 | 32.1 | 639 | 1 | AL896412 |
| C 35 | 17 | 32.1 | 669 | 1 | AL651847 |
| C 36 | 17 | 32.1 | 687 | 9 | AG179628 |
| C 37 | 17 | 32.1 | 703 | 6 | CA259339 |
| C 38 | 17 | 32.1 | 720 | 7 | CK183518 |
| C 39 | 17 | 32.1 | 720 | 9 | BX240998 |
| C 40 | 17 | 32.1 | 824 | 8 | CC431250 |
| C 41 | 17 | 32.1 | 844 | 8 | CC407226 |
| C 42 | 17 | 32.1 | 846 | 9 | CL563987 |
| C 43 | 17 | 32.1 | 930 | 8 | BZ667152 |
| C 44 | 17 | 32.1 | 973 | 3 | AY068889 |
| C 45 | 17 | 32.1 | 980 | 9 | CNS0630W |

ALIGNMENTS

RESULT 1
BM067231/c 127 bp mRNA linear EST 11-SEP-2002
LOCUS KS08001E12 KS08 Capsicum annuum cDNA, mRNA sequence.
DEFINITION BM067231
ACCESSION BM067231.1 GI:22787366
VERSION
KEYWORDS
SOURCE
ORGANISM
EST

Capsicum annuum
Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Capsicum.

REFERENCE
1 (bases 1 to 127)
Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S.,
Hur, C.-G. and Choi, D.
Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
annuum L.) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen

JOURNAL
COMMENT
Contact: Doil Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doil@mail.kribb.re.kr
High quality sequence stop: 127.
Location/Qualifiers

FEATURES

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/cuiivar="Hang Keun"
/db_xref="taxon:4072"
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/note="Vector: pBluescript SK(-)"

ORIGIN

Query Match 84.9% Score 45; DB 4; Length 127;
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Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
5 CATGACAAATCTGAATACCAAGTGTGTCGTAACCGTGATG 49
79 CATGACAAATCTGAATACCAAGTGTGTCGTAACCGTGATG 35

date note

RESULT 2
 BBA40162 287 bp mRNA linear EST 19-JUL-2000
 DEFINITION BBA40162 RIKEN full-length enriched, 9 days embryo Mus musculus
 cDNA clone DO30020106 3' similar to U19312 Mouse (beta Ig-h3) mRNA,
 mRNA sequence.
 ACCESSION BBA40162
 VERSION BBA40162.1 GI:9282774
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 287)
 REFERENCE Konomi,H., Aizawa,K., Akahata,S., Akiyama,J., Arakawa,T.,
 Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
 Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
 Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
 Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
 Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
 Shibata,K., Shibata,Y., Shigemoto,Y., Shingawa,A., Shiiki,T.,
 Sogabe,Y., Suganara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
 Takahashi,F., Tomimaga,N., Toya,T., Tsunoda,Y., Watabiki,A.,
 Watanabe,S., Yamamura,T., Yamanaoka,I., Yano,R., Yasunishi,A.,
 Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
 Hayashizaki,Y.
 RIKEN Mouse ESTs (Konomi,H., et al.)
 Unpublished (2000)
 COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9226
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagoka,S.,
 Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermostabilization and thermooactivation of thermostable enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh,M., Kikunishi,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
 Okazaki,Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.etc.riken.go.jp>) for
 further details.
 FEATURES
 SOURCE Location/Qualifiers
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 /mol_type="mRNA"
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 /lab_host="DH10B"
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 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5',
 GAGGAGAGACGGCCGACACCGAGTTTGTGTTTGTGTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the

| Query Match | 37.7% | Score 20 | DB 2 | Length 287 |
|--|----------------|---------------|----------|------------|
| Best Local Similarity | 100.0% | Prod. No. 1.3 | | |
| Matches 20 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| <p>10 ACAATCTGAATCAACAGT 29</p> <p>47 ACAATCTGAATCAACAGT 66</p> | | | | |
| <p>BB006007 288 bp mRNA linear EST 22-JUN-2000</p> <p>BB006007 RIKEN full-length enriched, 10 day neonate skin Mus</p> <p>musculus cDNA clone 473246FP4.3, ssimilar to NM_009369 Mus musculus</p> <p>transforming growth factor, beta induced, 68 kDa (Tgfb1), mRNA</p> <p>sequence.</p> <p>BB006007</p> <p>BB006007.1 GI:8095422</p> <p>EST.</p> <p>Mus musculus (house mouse)</p> <p>Mus musculus</p> <p>Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p> <p>Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.</p> <p>1 (bases 1 to 288)</p> <p>Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,</p> <p>Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,</p> <p>Ihazane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,</p> <p>Iizawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,</p> <p>Kiyosawa, K., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,</p> <p>Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,</p> <p>Ozaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,</p> <p>Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,</p> <p>Sogabe, Y., Suganara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,</p> <p>Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Watanishi, A.,</p> <p>Watanabe, S., Yamamura, T., Yamana, I., Yano, R., Yasunishi, A.,</p> <p>Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and</p> <p>Hayashizaki, Y.</p> <p>RIKEN Mouse ESTs (Konno, H., et al.)</p> <p>Unpublished (2000)</p> <p>Contact: Yoshihide Hayashizaki</p> <p>Laboratory for Genome Exploration Research Group, RIKEN Genomic</p> <p>Sciences Center (GSC), Yokohama Institute</p> <p>The Institute of Physical and Chemical Research (RIKEN)</p> <p>1-7-22 Suenho-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan</p> <p>Tel: 81-45-503-9222</p> <p>Fax: 81-45-503-9216</p> <p>Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/</p> <p>Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagoka, S.,</p> <p>Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.</p> <p>Thermosensitization and thermoregulation of thermolabile enzymes by</p> <p>trehalose and its application for the syntheses of full length</p> <p>cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)</p> <p>Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,</p> <p>Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,</p> <p>Okazaki, Y. and Hayashizaki, Y.</p> <p>Automated filtration-based high-throughput plasmid preparation</p> <p>system. Genome Res. 9 (5), 463-470 (1999)</p> <p>Carninci, P. and Hayashizaki, Y.</p> <p>High-efficiency full-length cDNA cloning. Methods Enzymol. 303,</p> <p>19-44 (1999)</p> <p>Please visit our web site (http://genome.riken.go.jp) for</p> <p>further details.</p> <p>Location/Qualifiers</p> <p>1..288</p> <p>/organism="Mus musculus"</p> <p>/mol_type="mRNA"</p> <p>/strain="C57BL/6J"</p> | | | | |

/db xref="taxon:10090"
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 /tissue_type="skin"
 /dev_stage="10 days neonate"
 /lab_host="DH10B"
 /clone_1ib="RIKEN full-length enriched, 10 day neonate skin"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5']
 GAGAGAGAGATTCGAGCTCTTTTCTTTTCTTTT 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'] GAGAGAGATTCGAGCTCTTTTCTTTTCTTTT 3'. cDNA was cloned into the XhoI and BamHI sites.
 Vector: a modified Bluescript KS(+) after bulk excision from lambda FLC I"

ORIGIN

Query Match 34.0%; Score 18; DB 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

10 ACAATCTGAATCAACCA 27
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 37 ACAATCTGAATCAACCA 54

Db

RESULT 4

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BB494132 316 bp mRNA linear EST 25-JUL-2000
 BB494132 RIKEN full-length enriched, 13 days embryo stomach Mus
 musculus cDNA clone D53003K16 3' similar to I19932 Mouse (beta
 1g-h3) mRNA, mRNA sequence.
 BB494132.1 GI:9452759
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 316)
 Komu,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
 Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
 Hirazane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
 Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,U., Kikuchi,N.,
 Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
 Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
 Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
 Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
 Takanashi,F., Tomimaga,N., Toya,T., Tsunoda,Y., Watanishi,A.,
 Watanabe,S., Yamamura,T., Yamana,I., Yano,R., Yasunishi,A.,
 Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M., and
 Hayashizaki,Y.
 RIKEN Mouse ESTs (Komu,H., et al.)
 Unpublished (2000)
 Contact: Yoshinide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/

FEATURES

source

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
 Saeki,N., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
 Thrombostabilization and thermooactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
 Itoh,M., Katsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
 Okazaki,Y., and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

Location/Qualifiers

1..316
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 /clone="D53003K16"
 /tissue_type="stomach"
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 /clone_1ib="RIKEN full-length enriched, 13 days embryo
 stomach"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN, Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5']
 GAGAGAGAGCGCCGCACTCGAGTTTCTTTTCTTTT 3', cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5']
 GAGAGAGATTCGAGCTCTTTTCTTTTCTTTT 3'. cDNA
 was cleaved with BamHI and XhoI. Vector: a modified
 Bluescript KS(+) after bulk excision from lambda FLC I."

ORIGIN

Query Match 34.0%; Score 18; DB 2; Length 316;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

10 ACAATCTGAATCAACCA 27
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 65 ACAATCTGAATCAACCA 82

Db

RESULT 5

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CA016832 428 bp mRNA linear EST 23-OCT-2002
 CA016832 Hordeum vulgare subsp. vulgare cDNA clone HV05N02
 3-PRIME, mRNA sequence.
 CA016832.1 GI:24294176
 EST.
 Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidae; Triticeae; Hordeum.
 1 (bases 1 to 428)
 Zhang,H., Pocockina,E., Michalek,W., Weschke,W., Stein,N. and
 Graner,A.
 Barley ESTs from germinating seeds
 Unpublished (2002)
 Contact: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)

Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
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 Location/Qualifiers

FEATURES
 source

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ORIGIN

Query Match 34.0%; Score 18; DB 6; Length 428;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 AATCTGAATCAACCACT 29
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 198 AATCTGAATCAACCACT 181

RESULT 6
 CA017649

LOCUS 500 bp mRNA linear EST 23-OCT-2002
 DEFINITION HV05N02r HV Hordeum vulgare subsp. vulgare cDNA clone HV05N02
 5-PRIME. mRNA sequence.

ACCESSION CA017649
 KEYWORDS GI:24294993

SOURCE EST.
 Hordeum vulgare subsp. vulgare

ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 500)
 Zhang, H., Potchikina, E., Michalek, W., Weschke, W., Stein, N. and Graner, A.

TITLE Barley ESTs from germinating seeds
 JOURNAL Unpublished (2002)

COMMENT Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert Length: 500 Std Error: 0.00
 Plate: 5 row: N column: 2
 Seq primer: M3rev.

FEATURES
 source

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/lab_host="XL10-Gold"
/clone_1ib="HV"
/notes="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA). Roots were grown for two days on filter paper at room temperature. Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable. Average insert size is 1 kb"
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ORIGIN

Query Match 34.0%; Score 18; DB 6; Length 500;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 AATCTGAATCAACCACT 29
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 452 AATCTGAATCAACCACT 469

RESULT 7
 BQ595418

LOCUS 597 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012691-024-022-C22-SP6 MP12-ADIS-024-developing root Beta vulgaris
 cDNA clone 024-022-C22 5-PRIME. mRNA sequence.

ACCESSION BQ595418
 VERSION BQ595418.1 GI:26125001

KEYWORDS EST.
 SOURCE Beta vulgaris

ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 597)
 Herwig, R., Schultz, B., Weisshaar, B., Hennig, S., Steinfaß, M.,
 Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
 and Radclouf, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 JOURNAL fingerprinting allows access to 25 000 potential sugar beet genes
 MEDLINE Plant J. 32 (5), 845-857 (2002)
 PUBMED 12472698

COMMENT Contract: Weisshaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Köln, Germany
 Fax: 00492215062851
 Email: weisshaar@ipk-koeln.mpg.de
 Insert Length: 597 Std Error: 0.00
 Plate: 22 row: C column: 22
 Seq primer: SP6; CATACGTTTAGGTGACACTATAG.

FEATURES
 source

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1..597
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:191436"
/db_xref="taxon:161934"
/clone="024-022-C22"
/issue_type="developing root"
/lab_host="EMDH108"
/clone_1ib="MP12-ADIS-024-developing root"
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/note="Vector: PCWSPORT6; Site_1: Sali; Site_2: NotI; cDNA library from sugar beet, library provided by KMS Kleinschleibner Saatzucht AG Rinbeck, Germany, contact: b.schulz@kms.de; cloning sites Sali-NotI, primer sites and orientation: 586-Sali-CCAGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN

Query Match 34.0%; Score 18; DB 5; Length 597;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AATCTGAATCAACCACTG 30
145 AATCTGAATCAACCACTG 162

RESULT 8
BM333093/c 608 bp mRNA linear EST 16-JAN-2002
LOCUS MEST183-H08.T3 ISUMS-RN Zea mays cDNA clone MEST183-H08 3', mRNA
DEFINITION sequence.
ACCESSION BM333093
VERSION BM333093.1 GI:18163254
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Wen, T.J., Qiu, F., Guo, L., Ashlock, D.A. and Schnable, P.S.
TITLE Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones
JOURNAL Unpublished (2001)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu

Individual basacall and confidence value were assigned using the phred software,
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#rt>). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<http://www.tigr.org/softlab/>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
1. 608

FEATURES
source
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST183-H08"
/issue_type="mixed"
/lab_host="DH10B"
/clone_lib="ISUMS-RN"
/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI; tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature tissues (17, 21, 38, 69, 77 DAG), Kernels

ORIGIN

Query Match 34.0%; Score 18; DB 4; Length 608;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATCAACCACTGCTG 34
317 TGAATCAACCACTGCTG 300

RESULT 9
BM347598/c 611 bp mRNA linear EST 16-JAN-2002
LOCUS MEST279-G08.T3 ISUMS-RN Zea mays cDNA clone MEST279-G08 3', mRNA
DEFINITION sequence.
ACCESSION BM347598
VERSION BM347598.1 GI:18172210
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Wen, T.J., Qiu, F., Guo, L., Ashlock, D.A. and Schnable, P.S.
TITLE Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones
JOURNAL Unpublished (2001)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu

Individual basacall and confidence value were assigned using the phred software,
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#rt>). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<http://www.tigr.org/softlab/>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)

(3, 5, 10, 15, 20, 25, 30, DAG), Adventitious roots (65 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a-Naphthalene acetic acid)-treated seedlings, Kinetin-treated seedlings, ACP (1-aminocyclopropane-1-carboxylic acid)-treated seedlings, Brassinolide-treated seedlings, ABA (abscisic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings, ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5', AACTGGAAGATTGGCGCGCGAGGATTTTCTTTT). The resulting DNA-RNA hybrid was treated with RNase H and used as a template for DNA pol-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcello Bento Soares (Genome Research 6: 791-806, 1996)."

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES
source
1..611
Location/Qualifiers

/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MES279-G08"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_id="ISUM5-RN"
/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI; tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels (3, 5, 10, 15, 20, 25, 30, 39, 49, 59, 69, 77 DAG), Tassel (3-39 cm, 53 and 56 DAG) Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a-Naphthalene acetic acid)-treated seedlings, Kinetin-treated seedlings, ACPG (1-aminocyclopropane-1-carboxylic acid)-treated seedlings, Brassinolide-treated seedlings, ABA (abscisic acid)-treated seedlings, GA (gibberellic acid)-treated seedlings, JA (jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5', AACTGGAAGATTCGCGCGCGAGAAATTTTCTTTTCTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcello Bento Soares (Genome Research 6: 791-806, 1996)."

ORIGIN

Query Match 34.0%; Score 18; DB 4; Length 611;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATCAACAGTCTGG 34
|||||
Db 320 TGAATCAACAGTCTGG 303

RESULT 10

AG223668 627 bp DNA linear GSS 19-JUL-2003
LOCUS AG223668
DEFINITION Lotus corniculatus var. japonicus DNA, clone:LB09d22_r, genomic survey sequence.

ACCESSION AG223668
VERSION AG223668.1 GI:26532397
KEYWORDS
SOURCE
ORGANISM Lotus corniculatus var. japonicus (Lotus japonicus)

Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.

REFERENCE

1 Sato, S., Nakamura, Y. and Tabata, S.
Lotus japonicus BAC End sequences
Published Only in Database (2002)
2 (bases 1 to 627)
Sato, S.
Direct Submission
Submitted (20-NOV-2002) Shusui Sato, Kazusa DNA Research Institute,
The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan

FEATURES
source
1..627
Location/Qualifiers
(E-mail: ssato@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/,
Tel: 81-438-52-3935 (ex. 2336), Fax: 81-438-52-3934)

/organism="Lotus corniculatus var. japonicus"
/mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/varietal="japonicus"
/db_xref="taxon:34305"
/clone="LJ1809d22_r"
/clone_id="genomic BAC library"
/note="VECTOR: pBelobAC11-synonym: Lotus japonicus"

ORIGIN

Query Match 34.0%; Score 18; DB 9; Length 627;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TCCATGACAAATCTGAA 20
|||||
Db 309 TCCATGACAAATCTGAA 326

RESULT 11
B1271889 629 bp mRNA linear EST 18-JUL-2001
LOCUS B1271889/c
DEFINITION NF014E05FL1038 Developing flower Medicago truncatula cDNA clone NF014E05FL 5', mRNA sequence.

ACCESSION B1271889
VERSION B1271889.1 GI:14880751
KEYWORDS
SOURCE
ORGANISM Medicago truncatula (barrel medic)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.

1 (bases 1 to 629)
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzalez, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula flower library
Unpublished (2001)

JOURNAL
COMMENT
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 224 6650
Fax: 580 224 6692
Email: gdmay@noble.org
Insert Length: 629 Std Error: 0.00
Plate: 014 row: E column: 05
Seq primer: TCACACAGAAACAGCTATGAC.

FEATURES
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1..629
Location/Qualifiers

/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF014E05FL"
/tissue_type="Developing flowers"
/dev_stage="Developmentally pooled. Contains a mixture of very young, developing, fully-opened flowers and flowers in early transition into pods."
/note="Vector: Lambda Zap; cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the GigaPack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExSist helper phage and the E. coli strain

ORIGIN XLI-Blue MRF[®] (Stratagene). Excised plasmids were plated using SOUR cells."

Query Match 34.0%; Score 18; DB 4; Length 629;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATCCATGACCAATCTG 18
|||||
Db 108 GATCCATGACCAATCTG 91

RESULT 12

LOCUS BX752014 688 bp mRNA linear EST 09-DEC-2003
DEFINITION BX752014 XGC-gastrula Xenopus tropicalis cDNA clone TGas076c13 3',
mRNA sequence.

ACCESSION BX752014
VERSION BX752014.1 GI:39642082
KEYWORDS EST
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis

REFERENCE 1 (bases 1 to 688)
AUTHORS Cronling,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT Contact: Cronling MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tlp@sanger.ac.uk

REFERENCE 1 (bases 1 to 688)
AUTHORS Cronling,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT Contact: Cronling MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tlp@sanger.ac.uk

REFERENCE 1 (bases 1 to 688)
AUTHORS Cronling,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT Contact: Cronling MDR
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tlp@sanger.ac.uk

FEATURES
source 1..688
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TGas076c13"
/dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XLI-blue"
/clone_1ib="XGC-gastrula"
/note="Vector: PCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into PCS107 with Vector: PCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XLI-blue.
location/Qualifiers

1..688
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TGas076c13"
/dev_stage="gastrula (stages 10.5-12 mixed)"
/lab_host="Escherichia coli XLI-blue"
/clone_1ib="XGC-gastrula"
/note="Vector: PCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into PCS107 with EcoRI at the 5' end and NotI at the 3' end."

ORIGIN
Query Match 34.0%; Score 18; DB 5; Length 688;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TCATGACCAATCTGAA 20
|||||
Db 332 TCATGACCAATCTGAA 349

RESULT 13
LOCUS CK185060 688 bp mRNA linear EST 01-JUL-2004
DEFINITION EST774375 BEA Boophilus microplus cDNA clone BEAC260, mRNA

sequence.
ACCESSION CK185060
VERSION CK185060.1 GI:49565594
KEYWORDS EST.
SOURCE Boophilus microplus (southern cattle tick)
ORGANISM Boophilus microplus

REFERENCE 1 (bases 1 to 688)
AUTHORS Nene,V., Quackenbush,J., George,J. and Guerrero,F.
TITLE An index of genes transcribed in the tick Boophilus microplus
JOURNAL Unpublished (2004)
COMMENT Other ESTs: EST774376
Contact: Vishwanath Nene
Parasite Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-610-5968
Fax: 301-838-0208
Email: nene@igr.org
Seq primer: M13 forward

FEATURES
source 1..688
/organism="Boophilus microplus"
/mol_type="mRNA"
/db_xref="taxon:6941"
/clone="BEAC260"
/dev_stage="Adult and larvae"
/lab_host="E. coli strain DH10B-Tona"
/clone_1ib="BEA"
/note="Organ: Whole ticks and dissected organs; Vector: pExpress 1; A normalized cDNA library was custom built by Express Genomics. Oligo-dt primed cDNA was directionally cloned into NotI-EcoRV site of pExpress 1. Universal M13 primers were used to generate 5' and 3' EST data."

ORIGIN
Query Match 34.0%; Score 18; DB 7; Length 688;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 34 GTCCGTAACCGTCGACGAG 51
|||||
Db 45 GTCCGTAACCGTCGACGAG 62

RESULT 14
LOCUS CB634510 701 bp mRNA linear EST 08-APR-2003
DEFINITION OSITEB14B06.f OSITEB Oryza sativa (indica cultivar-group) cDNA clone OSITEB14B06 5', mRNA sequence.
ACCESSION CB634510
VERSION CB634510.1 GI:29629501
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)

REFERENCE 1 (bases 1 to 701)
AUTHORS Jantaasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wang,R. and Wang,G.
TITLE large-scale identification of ESTs involved in the interaction between rice and Magnaporthe oryzae
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

PCR Primers
 FORWARD: gta aac cga cgg cca gtc
 BACKWARD: gga aac agc tat gac cat g
 Plate: 14 row: B column: 06
 Seq primer: gta aac cga cgg cca gtc.

FEATURES
 source
 1..701
 Location/Qualifiers

/organism="Oryza sativa (indica cultivar-group)"
 /mol_type="rRNA"
 /cultivar="IR36"
 /db_xref="taxon:39946"
 /clone="OSIIEB14B05"
 /tissue_type="Leaf"
 /dev_stage="3 week"
 /lab_host="DH10B"
 /clone_1ib="OSIIEB"
 /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
 XhoI; 24 hrs after inoculation with Rice Blast (Poe-6-3)"

ORIGIN

Query Match 34.0%; Score 18; DB 6; Length 701;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ATGACAAATCTGAATCA 23
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 Db 586 ATGACAAATCTGAATCA 569

RESULT 15

CC501966 713 bp DNA linear GSS 17-JUN-2003
 CH240_340H21.T7 CHORI-240 Bos taurus genomic clone CH240_340H21,
 genomic survey sequence.

CC501966
 CC501966.1 GI:31820259

KEYWORDS

GSS.

SOURCE

Bos taurus (cow)
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE

AUTHORS

1 (bases 1 to 713)
 Holt,R., Scott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
 Tsai,M., Cloutier,A., Lee,D., Gilm,N., Olson,T., Mayo,M.,
 Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
 Mathewson,C., Mye,N., Masson,A., Brown-John,M., Jones,S.,
 Schein,J., Marra,M., de Jong,P., McMilliam,S., Barris,W.,
 Dalrymple,B.P. and Tellam,R.
 Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
 Unpublished (2003)
 Other GSSs: CH240_340H21.TARBAC13P2
 Contact: Rob Holt

TITLE

JOURNAL

COMMENT

Sequencing
 The British Columbia Cancer Agency Genome Science Centre
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
 Tel: 604-877-6085
 Fax: 604-877-6276

Email: rholt@ccgsc.ca

Clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering/information.htm). This work
 was undertaken as part of the International Bovine BAC Mapping
 Consortium (IBMC) by CSIRO Livestock Industries, Australia and the
 British Columbia Genome Sciences Centre, Canada.
 Plate: 340 row: H column: 21
 Seq primer: T7

FEATURES

source

1..713
 Location/Qualifiers
 /organism="Bos taurus"

ORIGIN

/mol_type="genomic DNA"
 /strain="bred: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_340H21"
 /sex="Male"
 /cell_type="Blood"
 /clone_1ib="CHORI-240"
 /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
 library (Male) produced by Pieter de Jong"

Query Match 34.0%; Score 18; DB 9; Length 713;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TGGACAAATCTGAATCAA 24
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 Db 413 TGGACAAATCTGAATCAA 396

Search completed: December 5, 2004, 07:59:11
 Job time : 1487 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 06:38:07 ; Search time 1425 Seconds
(without alignments)
1758.845 Million cell updates/sec

Title: US-09-857-841-3

Perfect score: 53
Sequence: 1 gatccatgacgaatctgaa.....gtcgtacgcgtcgacgagct 53

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size: 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

GenEmbl:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match length | ID | Description |
|------------|-------|--------------------|-----|-------------|
| 1 | 53 | 100.0 | 53 | BD261798 |
| 2 | 46 | 86.8 | 771 | AR111976 |
| 3 | 46 | 86.8 | 772 | AR111981 |
| 4 | 45 | 84.9 | 130 | AR031575 |
| 5 | 45 | 84.9 | 130 | AR031575 |
| 6 | 45 | 84.9 | 130 | AR065687 |
| 7 | 45 | 84.9 | 130 | AR097446 |
| 8 | 45 | 84.9 | 130 | AR097446 |
| 9 | 45 | 84.9 | 131 | AR031572 |
| 10 | 45 | 84.9 | 131 | AR065684 |
| 11 | 45 | 84.9 | 131 | AR097443 |
| 12 | 45 | 84.9 | 131 | AR097443 |
| 13 | 45 | 84.9 | 152 | AR031570 |
| 14 | 45 | 84.9 | 152 | AR065682 |
| 15 | 45 | 84.9 | 152 | AR097441 |
| 16 | 45 | 84.9 | 152 | AR097441 |
| 17 | 45 | 84.9 | 154 | AR031574 |
| 18 | 45 | 84.9 | 154 | AR065686 |
| 19 | 45 | 84.9 | 154 | AR097445 |

| | | | | | | |
|----|----|------|------|----|-----------|--------------------|
| 20 | 45 | 84.9 | 154 | 6 | 149963 | 149963 Sequence 13 |
| 21 | 45 | 84.9 | 862 | 14 | CMU32859 | U32859 Cucurbit mo |
| 22 | 45 | 84.9 | 864 | 14 | CMU32858 | U32858 Cucurbit mo |
| 23 | 45 | 84.9 | 894 | 14 | MCVCPB | 136525 Cucurbit mo |
| 24 | 45 | 84.9 | 976 | 6 | A32131 | A32131 CMV capsid |
| 25 | 45 | 84.9 | 976 | 6 | AR021486 | AR021486 Sequence |
| 26 | 45 | 84.9 | 976 | 6 | AR138342 | AR138342 Sequence |
| 27 | 45 | 84.9 | 976 | 6 | AR364710 | AR364710 Sequence |
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| 37 | 45 | 84.9 | 1043 | 14 | CMU2821 | U2821 Cucurbit mo |
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ALIGNMENTS

RESULT 1

BD261798

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

ORIGIN

Query Match

Best Local Similarity

Matches

1 GATCATGACGAATCTGAATCAACGAGTGTGCTGTAACCGTCGACGAGCT 53

QY

Db 1 GATCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACGACT 53
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LOCUS AR111976 771 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6127601.
ACCESSION AR111976
VERSION AR111976.1 GI:12828824
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 771)
Boeshore,M.L., McMaster,R.J., Triccoli,D.M., Reynolds,J.F. and
Carney,K.J.
TITLE Plants resistant to C strains of cucumber mosaic virus
JOURNAL Patent: US 6127601-A 5 03-OCT-2000;
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
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Db 1 CCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 46
RESULT 3
AR111981
LOCUS AR111981 772 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 14 from patent US 6127601.
ACCESSION AR111981
VERSION AR111981.1 GI:12828829
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 772)
Boeshore,M.L., McMaster,R.J., Triccoli,D.M., Reynolds,J.F. and
Carney,K.J.
TITLE Plants resistant to C strains of cucumber mosaic virus
JOURNAL Patent: US 6127601-A 14 03-OCT-2000;
FEATURES
Location/Qualifiers
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RESULT 4
AR111975
LOCUS AR111975 792 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6127601.
ACCESSION AR111975
VERSION AR111975.1 GI:12828823
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 792)
Boeshore,M.L., McMaster,R.J., Triccoli,D.M., Reynolds,J.F. and
Carney,K.J.
TITLE Plants resistant to C strains of cucumber mosaic virus
JOURNAL Patent: US 6127601-A 3 03-OCT-2000;
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AR031575
LOCUS AR031575 130 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5866384.
ACCESSION AR031575
VERSION AR031575.1 GI:5945864
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 130)
Haeeloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 14 02-FEB-1999;
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RESULT 6
AR065687
LOCUS AR065687 130 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5849548.
ACCESSION AR065687
VERSION AR065687.1 GI:5995903
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 130)
Haeeloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 14 15-DEC-1998;
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/mol_type="unassigned DNA"
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Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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52 CATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 96

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RESULT 7
LOCUS AR097446 130 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 14 from patent US 6071730.
ACCESSION AR097446
VERSION AR097446.1 GI:12806176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 14 06-JUN-2000;
FEATURES Location/Qualifiers
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52 CATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 96

DB

RESULT 8
LOCUS 149964 130 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 14 from patent US 5641673.
ACCESSION 149964
VERSION 149964.1 GI:2472184
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5641673-A 14 24-JUN-1997;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.3e-15;
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DB

RESULT 9
LOCUS AR031572 131 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5866384.
ACCESSION AR031572
VERSION AR031572.1 GI:5945861
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 11 02-FEB-1999;
FEATURES Location/Qualifiers
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DB

RESULT 10
LOCUS AR065684 131 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5849548.
ACCESSION AR065684
VERSION AR065684.1 GI:5995900
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 11 15-DEC-1998;
FEATURES Location/Qualifiers
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DB

RESULT 11
LOCUS AR097443 131 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6071730.
ACCESSION AR097443
VERSION AR097443.1 GI:12806173
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 11 06-JUN-2000;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Db | 53 | CATGGACAAATCTGATCAACACGAGCTGCTGTAACCGTGCAGC | 97 | | |
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| LOCUS | 149961 | | 131 bp | DNA | linear |
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| ACCESSION | 149961 | | | | |
| VERSION | 149961.1 | GI:2472181 | | | |
| KEYWORDS | | | | | |
| SOURCE | | | | | |
| ORGANISM | Unknown. | | | | |
| REFERENCE | Unclassified. | | | | |
| 1 | (bases 1 to 131) | | | | |
| AUTHORS | Haeleloff,J., Brand,A., Perrimon,N. and Goodman,H.M. | | | | |
| TITLE | Cell ablation using trans-splicing ribozymes | | | | |
| JOURNAL | Patent: US 5641673-A 11 24-JUN-1997; | | | | |
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| RESULT 13 | | | | | |
| LOCUS | AR031570 | | 152 bp | DNA | linear |
| DEFINITION | Sequence 9 from patent US 5866384. | | | | PAT 29-SEP-1999 |
| ACCESSION | AR031570 | | | | |
| VERSION | AR031570.1 | GI:5945859 | | | |
| KEYWORDS | | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unknown. | | | | |
| REFERENCE | Unclassified. | | | | |
| 1 | (bases 1 to 152) | | | | |
| AUTHORS | Haeleloff,J., Brand,A., Perrimon,N. and Goodman,H.M. | | | | |
| TITLE | Cell ablation using trans-splicing ribozymes | | | | |
| JOURNAL | Patent: US 5866384-A 9 02-SEP-1999; | | | | |
| FEATURES | Location/Qualifiers | | | | |
| Source | 1..152 | | | | |
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| DEFINITION | Sequence 9 from patent US 5849548. | | | | PAT 29-SEP-1999 |
| ACCESSION | AR065682 | | | | |
| VERSION | AR065682.1 | GI:5995898 | | | |
| KEYWORDS | | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unknown. | | | | |
| | Unclassified. | | | | |

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REFERENCE
AUTHORS      1 (bases 1 to 152)
TITLE        Hasei-Loeff,J., Brand,A., Perrimon,N. and Goodman,H.M.
JOURNAL      Cell ablation using trans-splicing ribozymes
FEATURES
source       Patent: US 5849548-A, 9 15-DEC-1998;
              Location/Qualifiers
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74 CATGGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 118

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DEFINITION    Sequence 9 from patent US 6071730.
ACCESSION     AR097441
VERSION       AR097441.1 GI:12806171
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unknown.
REFERENCE
1 (bases 1 to 152)
AUTHORS      Hasei-Loeff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE        Cell ablation using trans-splicing ribozymes
JOURNAL      Patent: US 6071730-A 9 06-JUN-2000;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 46 | 86.8 | 772 | 13 | US-10-011-033-14 |
| 3 | 46 | 86.8 | 792 | 13 | US-10-011-033-3 |
| 4 | 43 | 81.1 | 772 | 13 | US-10-011-033-1 |
| 5 | 37 | 69.8 | 960 | 13 | US-10-011-033-9 |
| 6 | 37 | 7.7 | 1674 | 15 | US-10-369-493-35833 |
| 7 | 30 | 34.0 | 1020 | 18 | US-10-425-115-38826 |
| 8 | 18 | 34.0 | 1116 | 15 | US-10-156-761-6291 |
| 9 | 18 | 34.0 | 1996 | 16 | US-10-424-599-94969 |
| 10 | 18 | 34.0 | 3878 | 14 | US-10-101-464A-950 |
| 11 | 18 | 34.0 | 9025608 | 15 | US-10-156-761-1 |
| 12 | 17 | 32.1 | 285 | 17 | US-10-437-963-97141 |

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| 13 | 17 | 32.1 | 762 | 13 | US-10-027-632-3534 | Sequence 3534, Ap |
| 14 | 17 | 32.1 | 762 | 13 | US-10-027-632-3535 | Sequence 3535, Ap |
| 15 | 17 | 32.1 | 762 | 13 | US-10-027-632-3536 | Sequence 3536, Ap |
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| 17 | 17 | 32.1 | 762 | 15 | US-10-027-632-3535 | Sequence 3535, Ap |
| 18 | 17 | 32.1 | 762 | 15 | US-10-027-632-3536 | Sequence 3536, Ap |
| 19 | 17 | 32.1 | 28854 | 9 | US-09-741-151-3 | Sequence 3, Appli |
| 20 | 16 | 30.2 | 527 | 17 | US-10-767-701-22640 | Sequence 22640, A |
| 21 | 16 | 30.2 | 707 | 16 | US-10-424-599-105422 | Sequence 105422, A |
| 22 | 16 | 30.2 | 713 | 13 | US-10-027-632-21126 | Sequence 21126, A |
| 23 | 16 | 30.2 | 713 | 13 | US-10-027-632-21126 | Sequence 21126, A |
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| 25 | 16 | 30.2 | 744 | 13 | US-10-027-632-20862 | Sequence 20862, A |
| 26 | 16 | 30.2 | 824 | 17 | US-10-767-701-5419 | Sequence 5419, Ap |
| 27 | 16 | 30.2 | 2621 | 16 | US-10-424-599-76572 | Sequence 76572, A |
| 28 | 16 | 30.2 | 4116 | 15 | US-10-296-540-3 | Sequence 3, Appli |
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| 30 | 16 | 30.2 | 11476 | 16 | US-10-434-893A-3 | Sequence 3, Appli |
| 31 | 15 | 28.3 | 145 | 9 | US-09-864-761-17367 | Sequence 17367, A |
| 32 | 15 | 28.3 | 246 | 18 | US-10-425-115-101455 | Sequence 101455, A |
| 33 | 15 | 28.3 | 390 | 17 | US-10-437-963-25065 | Sequence 25065, A |
| 34 | 15 | 28.3 | 402 | 17 | US-10-437-963-74167 | Sequence 74167, A |
| 35 | 15 | 28.3 | 419 | 17 | US-10-767-795-560 | Sequence 560, App |
| 36 | 15 | 28.3 | 441 | 18 | US-10-425-115-90059 | Sequence 90059, A |
| 37 | 15 | 28.3 | 449 | 14 | US-10-060-036-3474 | Sequence 3474, Ap |
| 38 | 15 | 28.3 | 449 | 14 | US-10-060-036-4108 | Sequence 4108, Ap |
| 39 | 15 | 28.3 | 472 | 16 | US-10-424-599-29886 | Sequence 29886, A |
| 40 | 15 | 28.3 | 480 | 11 | US-09-876-143-658 | Sequence 658, App |
| 41 | 15 | 28.3 | 508 | 15 | US-10-029-386-1276 | Sequence 1276, Ap |
| 42 | 15 | 28.3 | 517 | 14 | US-10-060-036-3938 | Sequence 3938, Ap |
| 43 | 15 | 28.3 | 517 | 17 | US-10-767-701-1327 | Sequence 1327, Ap |
| 44 | 15 | 28.3 | 520 | 13 | US-10-027-632-18852 | Sequence 18852, A |
| 45 | 15 | 28.3 | 520 | 15 | US-10-027-632-18852 | Sequence 18852, A |

ALIGNMENTS

RESULT 1
US-10-011-033-5
; Sequence 5, Application US/10011033
; Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L.
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber mosaic virus
STRAIN: V-34
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
OTHER INFORMATION: /codon_start=3
/function= "ENCAPSIDATES VIRUS RNA"
/product= "COAT PROTEIN"
/gene= "CP"
/number= 1
/standard_name= "COAT PROTEIN"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-011-033-5

Query Match 86.8%; Score 46; DB 13; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGACAAATCTGAATCAACCACTGCTGCTGCTAACCCTGCAGC 49
DB 1 CCATGACAAATCTGAATCAACCACTGCTGCTGCTAACCCTGCAGC 46

RESULT 2

US-10-011-033-14
Sequence 14, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: A35
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-011-033-14

Query Match 86.8%; Score 46; DB 13; Length 772;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCATGACAAATCTGAATCAACCACTGCTGCTGCTAACCCTGCAGC 49
DB 1 CCATGACAAATCTGAATCAACCACTGCTGCTGCTAACCCTGCAGC 46

RESULT 3

US-10-011-033-3
Sequence 3, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS

STRAIN: v-33
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-011-033-3

Query Match 86.8%; Score 46; DB 13; Length 792;
Best Local Similarity 100.0%; Pred. No. 1,7e-16;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCATGACAAATCTGAATCAACCAAGTCTGCTGTACCGTGAACG 49
1 CCATGACAAATCTGAATCAACCAAGTCTGCTGTACCGTGAACG 46

RESULT 4
US-10-011-033-1
Sequence 1, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J

TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lisa V. Mueller
TELEPHONE: 312-616-5400

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5460

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

MOLECULE TYPE: linear
HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: V-27

FEATURE:
NAME/KEY: CDS
LOCATION: 3..660

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-011-033-1

Query Match 81.1%; Score 43; DB 13; Length 772;
Best Local Similarity 100.0%; Pred. No. 8.9e-15;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 CCATGACAAATCTGAATCAACCAAGTCTGCTGTACCGTGAACG 46
1 CCATGACAAATCTGAATCAACCAAGTCTGCTGTACCGTGAACG 43

RESULT 5
US-10-011-033-9
Sequence 9, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J

TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lisa V. Mueller
TELEPHONE: 312-616-5400

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5460

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

MOLECULE TYPE: linear
HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: STRAIN C

FEATURE:
NAME/KEY: CDS
LOCATION: 1..658

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-011-033-9

Query Match 69.8%; Score 37; DB 13; Length 960;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ATGACAAATCTGAATCAACCAAGTCTGCTGTACCGTGAACG 42
1 ATGACAAATCTGAATCAACCAAGTCTGCTGTACCGTGAACG 37

RESULT 6
US-10-369-493-35833/c

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Sequence 35833, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10152052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35833
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35833

Query Match
Best Local Similarity 37.7%; Score 20; DB 15; Length 1674;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 28 GTGCTGGTGTACCGTCGA 47
Db 1278 GTGCTGGTGTACCGTCGA 1259

RESULT 7
US-10-425-115-38826
; Sequence 38826, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 38826
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_135411C.1
US-10-425-115-38826

Query Match
Best Local Similarity 34.0%; Score 18; DB 18; Length 1020;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 TGATCAACCGTGTGG 34
Db 983 TGAATCAACCGTGTGG 1000

RESULT 8
US-10-156-761-6291/c
; Sequence 6291, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
```

```
APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6291
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1116)
US-10-156-761-6291

Query Match
Best Local Similarity 34.0%; Score 18; DB 15; Length 1116;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 29 TGCTGTGTGTACCGTCG 46
Db 185 TGCTGTGTGTACCGTCG 168

RESULT 9
US-10-424-599-94969
; Sequence 94969, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 94969
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_56769C.1
US-10-424-599-94969

Query Match
Best Local Similarity 34.0%; Score 18; DB 16; Length 1996;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 33 GGTGTAACCGTCGACGA 50
Db 532 GGTGTAACCGTCGACGA 549

RESULT 10
US-10-101-464A-950/c
; Sequence 950, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
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; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 950
; LENGTH: 3878
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; US-10-101-464A-950

Query Match
Best Local Similarity 100.0%; Score 18; DB 14; Length 3878;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATGACAAATCTGAATCA 23
DB 2685 ATGACAAATCTGAATCA 2688

RESULT 11
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
; US-10-156-761-1

Query Match
Best Local Similarity 100.0%; Score 18; DB 15; Length 9025608;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TCGTGTCTGTAACCGTCG 46
DB 7582185 TCGTGTCTGTAACCGTCG 7582202

RESULT 12
US-10-437-963-97141
; Sequence 97141, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

```

; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 97141
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) ..(285)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95173C.1
; US-10-437-963-97141

Query Match
Best Local Similarity 100.0%; Score 17; DB 17; Length 285;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATCCATGACCAATCT 17
DB 255 GATCCATGACCAATCT 271

RESULT 13
US-10-027-632-3534
; Sequence 3534, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3534
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-3534

Query Match
Best Local Similarity 100.0%; Score 17; DB 13; Length 762;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AAATCTGATCAACCAG 28
DB 474 AAATCTGATCAACCAG 490
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```

RESULT 14
US-10-027-632-3535
; Sequence 3535, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3535
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-3535

```

```

Query Match      32.1%; Score 17; DB 13; Length 762;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      12 AAATCTGAATCAACCAG 28
Db      474 AAATCTGAATCAACCAG 490

```

```

RESULT 15
US-10-027-632-3536
; Sequence 3536, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3536
; LENGTH: 762

```

```

; TYPE: DNA
; ORGANISM: Human
US-10-027-632-3536
Query Match      32.1%; Score 17; DB 13; Length 762;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      12 AAATCTGAATCAACCAG 28
Db      474 AAATCTGAATCAACCAG 490

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Search completed: December 5, 2004, 08:04:09
Job time : 235 secs

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 03:53:58 : Search time 53 Seconds

(without alignments)
710.789 Million cell updates/sec

Title: US-09-857-841-3

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Gap: 10.0, Gapext 1.0 53

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents NA:*

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6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 46 | 86.8 | 771 | 3 | US-08-875-233-5 |
| 2 | 46 | 86.8 | 772 | 3 | US-08-875-233-14 |
| 3 | 46 | 86.8 | 792 | 3 | US-08-875-233-3 |
| 4 | 45.8 | 86.4 | 130 | 1 | US-08-090-193-14 |
| 5 | 45.8 | 86.4 | 130 | 2 | US-08-488-031-14 |
| 6 | 45.8 | 86.4 | 130 | 2 | US-08-486-569-14 |
| 7 | 45.8 | 86.4 | 130 | 2 | US-08-486-027-14 |
| 8 | 45.8 | 86.4 | 130 | 2 | US-08-090-192-14 |
| 9 | 45.8 | 86.4 | 130 | 2 | US-08-482-663-14 |
| 10 | 45.8 | 86.4 | 130 | 3 | US-08-482-658-14 |
| 11 | 45.8 | 86.4 | 130 | 3 | US-08-470-349-14 |
| 12 | 45.8 | 86.4 | 130 | 3 | US-08-475-610-14 |
| 13 | 45.8 | 86.4 | 130 | 5 | PCT-US92-00277-14 |
| 14 | 45.8 | 86.4 | 130 | 5 | PCT-US92-00278-14 |
| 15 | 45.8 | 86.4 | 131 | 1 | US-08-090-193-11 |
| 16 | 45.8 | 86.4 | 131 | 2 | US-08-488-031-11 |
| 17 | 45.8 | 86.4 | 131 | 2 | US-08-486-569-11 |
| 18 | 45.8 | 86.4 | 131 | 2 | US-08-488-027-11 |
| 19 | 45.8 | 86.4 | 131 | 2 | US-08-090-192-11 |
| 20 | 45.8 | 86.4 | 131 | 2 | US-08-482-663-11 |
| 21 | 45.8 | 86.4 | 131 | 3 | US-08-482-658-11 |
| 22 | 45.8 | 86.4 | 131 | 3 | US-08-470-349-11 |
| 23 | 45.8 | 86.4 | 131 | 3 | US-08-475-610-11 |
| 24 | 45.8 | 86.4 | 131 | 5 | PCT-US92-00277-11 |
| 25 | 45.8 | 86.4 | 131 | 5 | PCT-US92-00278-11 |
| 26 | 45.8 | 86.4 | 152 | 1 | US-08-090-193-9 |
| 27 | 45.8 | 86.4 | 152 | 2 | US-08-488-031-9 |

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| 28 | 45.8 | 86.4 | 152 | 2 | US-08-486-569-9 | Sequence 9, Appli |
| 29 | 45.8 | 86.4 | 152 | 2 | US-08-488-027-9 | Sequence 9, Appli |
| 30 | 45.8 | 86.4 | 152 | 2 | US-08-090-192-9 | Sequence 9, Appli |
| 31 | 45.8 | 86.4 | 152 | 2 | US-08-482-663-9 | Sequence 9, Appli |
| 32 | 45.8 | 86.4 | 152 | 3 | US-08-482-658-9 | Sequence 9, Appli |
| 33 | 45.8 | 86.4 | 152 | 3 | US-08-470-349-9 | Sequence 9, Appli |
| 34 | 45.8 | 86.4 | 152 | 3 | US-08-475-610-9 | Sequence 9, Appli |
| 35 | 45.8 | 86.4 | 152 | 5 | PCT-US92-00277-9 | Sequence 9, Appli |
| 36 | 45.8 | 86.4 | 154 | 1 | US-08-090-193-13 | Sequence 13, Appli |
| 37 | 45.8 | 86.4 | 154 | 2 | US-08-488-031-13 | Sequence 13, Appli |
| 38 | 45.8 | 86.4 | 154 | 2 | US-08-486-569-13 | Sequence 13, Appli |
| 39 | 45.8 | 86.4 | 154 | 2 | US-08-488-027-13 | Sequence 13, Appli |
| 40 | 45.8 | 86.4 | 154 | 2 | US-08-090-192-13 | Sequence 13, Appli |
| 41 | 45.8 | 86.4 | 154 | 2 | US-08-482-663-13 | Sequence 13, Appli |
| 42 | 45.8 | 86.4 | 154 | 3 | US-08-482-658-13 | Sequence 13, Appli |
| 43 | 45.8 | 86.4 | 154 | 3 | US-08-470-349-13 | Sequence 13, Appli |
| 44 | 45.8 | 86.4 | 154 | 3 | US-08-475-610-13 | Sequence 13, Appli |
| 45 | 45.8 | 86.4 | 154 | 5 | PCT-US92-00277-13 | Sequence 13, Appli |

ALIGNMENTS

RESULT 1
US-08-875-233-5
Sequence 5, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Steetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60689
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26/JUN/1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber mosaic virus
STRAIN: V-34
FEATURE:
NAME/KEY: CDS
LOCATION: 3...660
OTHER INFORMATION: /codon start=3
OTHER INFORMATION: /function= "ENCAPSIDATES VIRUS RNA"

OTHER INFORMATION: /product= "COAT PROTEIN"
OTHER INFORMATION: /gene= "Cp"
OTHER INFORMATION: /number= 1
OTHER INFORMATION: /standard_name= "COAT PROTEIN"
US-08-875-233-5

Query Match 86.8%; Score 46; DB 3; Length 771;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCATGACAAATCTGAATCAACCAAGTCTGTGCTTAACCGTCGACG 49
DB 1 CCATGACAAATCTGAATCAACCAAGTCTGTGCTTAACCGTCGACG 46

RESULT 2

US-08-875-233-14
Sequence 14, Application US/08875233

GENERAL INFORMATION:
PATENT No. 6127601
APPLICANT: Boeshore, Maury L.
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M.
APPLICANT: Reynolds, John F.
APPLICANT: Carney, Kim J.
TITLE OF INVENTION: Plants Resistant to C Strains of
CUCUMBER MOSAIC VIRUS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Steetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60689

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: A35
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660

US-08-875-233-14

Query Match 86.8%; Score 46; DB 3; Length 772;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCATGACAAATCTGAATCAACCAAGTCTGTGCTTAACCGTCGACG 49
DB 1 CCATGACAAATCTGAATCAACCAAGTCTGTGCTTAACCGTCGACG 46

RESULT 3

US-08-875-233-3
Sequence 3, Application US/08875233

GENERAL INFORMATION:
PATENT No. 6127601
APPLICANT: Boeshore, Maury L.
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M.
APPLICANT: Reynolds, John F.
APPLICANT: Carney, Kim J.
TITLE OF INVENTION: Plants Resistant to C Strains of
CUCUMBER MOSAIC VIRUS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Steetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60689

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: v-33
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660

US-08-875-233-3

Query Match 86.8%; Score 46; DB 3; Length 792;
Best Local Similarity 100.0%; Pred. No. 4.9e-09;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCATGACAAATCTGAATCAACCAAGTCTGTGCTTAACCGTCGACG 49
DB 1 CCATGACAAATCTGAATCAACCAAGTCTGTGCTTAACCGTCGACG 46

RESULT 4

US-08-090-193-14
Sequence 14, Application US/08090193

GENERAL INFORMATION:
PATENT No. 5641673
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5641673bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
;; STREET: 1100 New York Avenue, Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/090,193
;; FILING DATE: 23-DEC-1993
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/00277
;; FILING DATE: 16-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/642,330
;; FILING DATE: 17-JAN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cimbal, Michele A.
;; REGISTRATION NUMBER: 33,851
;; REFERENCE/DOCKET NUMBER: 0609.3080001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 130 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;;
US-08-090-193-14
;;
Query Match 86.4%; Score 45.8; DB 1; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;;
Qy 1 GATCCATGACAAATCTGAATCAACCACTGCTGCTGAACCGTCGACG 49
Db 48 GAGTCATGACAAATCTGAATCAACCACTGCTGCTGAACCGTCGACG 96
;;
RESULT 5
US-08-488-031-14
;; Sequence 14, Application US/08488031
;; Patent No. 5849548
;; GENERAL INFORMATION:
;; APPLICANT: Haseloff, James
;; APPLICANT: Brand, Andrea
;; APPLICANT: Peritmon, No. 5849548bert
;; APPLICANT: Goodman, Howard M.
;; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
;; STREET: 1100 New York Avenue, N.W., Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/488,031
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/090,193
;; FILING DATE: 23-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/00277
;; FILING DATE: 16-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/642,330
;; FILING DATE: 17-JAN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bugalsky, Lawrence B.
;; REGISTRATION NUMBER: 35,086
;; REFERENCE/DOCKET NUMBER: 0609.3080002/MAC/LBB
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 130 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: linear
;;
US-08-488-031-14
;;
Query Match 86.4%; Score 45.8; DB 2; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;;
Qy 1 GATCCATGACAAATCTGAATCAACCACTGCTGCTGAACCGTCGACG 49
Db 48 GAGTCATGACAAATCTGAATCAACCACTGCTGCTGAACCGTCGACG 96
;;
RESULT 6
US-08-486-569-14
;; Sequence 14, Application US/08486569
;; Patent No. 5863774
;; GENERAL INFORMATION:
;; APPLICANT: Haseloff, James
;; APPLICANT: Brand, Andrea
;; APPLICANT: Peritmon, No. 5863774bert
;; APPLICANT: Goodman, Howard M.
;; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
;; STREET: 1100 New York Avenue, N.W., Suite 600
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,569
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/090,193
;; FILING DATE: 23-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/00277
;; FILING DATE: 16-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/642,330
;; FILING DATE: 17-JAN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bugalsky, Lawrence B.
;; REGISTRATION NUMBER: 35,086
;; REFERENCE/DOCKET NUMBER: 0609.3080006/MAC/LBB
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
US-08-486-569-14

Query Match 86.4%; Score 45.8; DB 2; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 49
DB 48 GAGTCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 96

RESULT 7
US-08-488-027-14
; Sequence 14, Application US/08488027
; Patent No. 5866384
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perrimon, No. 5866384bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488.027
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/090.193
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 07/642.330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3080003/MAC/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
US-08-488-027-14

US-08-488-027-14

Query Match 86.4%; Score 45.8; DB 2; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 49

Db 48 GAGTCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 96

RESULT 8
US-08-090-192-14
; Sequence 14, Application US/08090192
; Patent No. 5874414
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090.192
; FILING DATE: 11-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/ US 92/00278
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642.333
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimdala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0609.3030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-090-192-14

Query Match 86.4%; Score 45.8; DB 2; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 49
DB 48 GAGTCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 96

RESULT 9
US-08-482-663-14
; Sequence 14, Application US/08482663
; Patent No. 5882907
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perrimon, No. 5882907bert
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600

US-08-482-663-14

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,663
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080005/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-482-663-14

Query Match 86.4%; Score 45.8; DB 2; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 48 GAGTCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 10
US-08-482-658-14
Sequence 14, Application US/08482658
Patent No. 6010904
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perlimon, No. 6010904bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193

FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080008/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-482-658-14

Query Match 86.4%; Score 45.8; DB 3; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 48 GAGTCATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 96

RESULT 11
US-08-470-349-14
Sequence 14, Application US/08470349
Patent No. 6015794
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,349
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,192
FILING DATE: 11-NOV-1993
APPLICATION NUMBER: PCT/ US 92/00278
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,333
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-470-349-14

Query Match 86.4%; Score 45.8; DB 3; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GATCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTGCAGC 49
DB 48 GAGTCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTGCAGC 96

RESULT 12

US-08-475-610-14
Sequence 14, Application US/08475610

PATENT No. 6071730

GENERAL INFORMATION:

APPLICANT: Haseloff, James

APPLICANT: Brand, Andrea

APPLICANT: Perlimon, No. 6071730bert

TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESS: Sterne, Kessler, Goldstein & Fox

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,610

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/090,193

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/00277

FILING DATE: 16-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/642,330

FILING DATE: 17-JAN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Bugalsky, Lawrence B.

REGISTRATION NUMBER: 35,086

REFERENCE/DOCKET NUMBER: 0609.3080004/MAC/LBB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 130 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

US-08-475-610-14

Query Match 86.4%; Score 45.8; DB 3; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GATCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTGCAGC 49
DB 48 GAGTCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTGCAGC 96

RESULT 13
PCT-US92-00277-14
Sequence 14, Application PC/RUS9200278

GENERAL INFORMATION:

APPLICANT: Haseloff, James

APPLICANT: Goodman, Howard M.

APPLICANT: Brand, Andrea

APPLICANT: Perlimon, Norbert

TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESS: Sterne, Kessler, Goldstein & Fox

STREET: 1225 Connecticut Avenue, N.W., Suite 300

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/00277

FILING DATE: 19920116

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/642,330

FILING DATE: 17-JAN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Goldstein, Jorge A

REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 0609.3496604

TELEPHONE: (202)833-7533

TELEFAX: (202)833-8716

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 130 bases

TYPE: NUCLEIC ACID

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA

PCT-US92-00277-14

Query Match 86.4%; Score 45.8; DB 5; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GATCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTGCAGC 49
DB 48 GAGTCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTGCAGC 96

RESULT 14
PCT-US92-00278-14
Sequence 14, Application PC/RUS9200278

GENERAL INFORMATION:

APPLICANT: Haseloff, James

APPLICANT: Goodman, Howard M.

TITLE OF INVENTION: Trans-Splicing Ribozymes

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESS: Sterne, Kessler, Goldstein & Fox

STREET: 1225 Connecticut Avenue, N.W., Suite 300

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00278
FILING DATE: 19920116
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,333
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3476604
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 833-7533
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Nucleic Acid
PCT-US92-00278-14

Query Match 86.4%; Score 45.8; DB 5; Length 130;
Best Local Similarity 95.9%; Pred. No. 3.6e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATCCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 49
48 GAGTCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 96

US-08-090-193-11
Sequence 11, Application US/08090193
Patent No. 5641673
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Peritimon, No. 5641673bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,193
FILING DATE: 23-DEC-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-090-193-11

Query Match 86.4%; Score 45.8; DB 1; Length 131;
Best Local Similarity 95.9%; Pred. No. 3.7e-09;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATCCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 49
49 GAGTCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 97

Search completed: December 5, 2004, 06:38:56
Job time: 53 secs

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| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 46 | 86.8 | 771 | 13 | US-10-011-033-5 | Sequence 5, Appl1 |
| 2 | 46 | 86.8 | 772 | 13 | US-10-011-033-14 | Sequence 14, Appl |
| 3 | 46 | 86.8 | 792 | 13 | US-10-011-033-3 | Sequence 3, Appl1 |
| 4 | 44.4 | 83.8 | 772 | 13 | US-10-011-033-1 | Sequence 1, Appl1 |
| 5 | 42.4 | 80.0 | 960 | 13 | US-10-011-033-9 | Sequence 9, Appl1 |
| 6 | 24.8 | 46.8 | 983 | 13 | US-10-011-033-11 | Sequence 11, Appl |
| 7 | 24 | 45.3 | 1068 | 8 | US-08-961-527-373 | GENERAL INFORM |
| 8 | 24 | 45.3 | 1068 | 16 | US-10-158-844-473 | Sequence 373, App |
| 9 | 23.6 | 44.5 | 352 | 16 | US-10-424-599-7715 | Sequence 373, App |
| 10 | 23.2 | 43.0 | 1680 | 15 | US-10-369-483-37626 | Sequence 7715, A |
| 11 | 22.8 | 43.0 | 662 | 10 | US-09-905-666A-20 | Sequence 37656, A |
| 12 | 22.8 | 43.0 | 766 | 17 | US-10-437-963-47739 | Sequence 20, Appl |
| | | | | | | Sequence 47739, A |

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| C | 13 | -22.6 | 42.6 | 2718 | 17 | US-10-437-963-34792 | A | Sequence 34792, App |
| C | 14 | -22.6 | 42.6 | 122859 | 13 | US-10-087-179-37 | A | Sequence 37, App |
| C | 15 | -22.6 | 42.6 | 536165 | 15 | US-09-933-964-1 | A | Sequence 1, App |
| C | 16 | -22.4 | 42.3 | 546 | 13 | US-10-027-632-200344 | A | Sequence 200344, Sequence 200344, |
| C | 17 | -22.4 | 42.3 | 546 | 15 | US-10-027-632-200344 | A | Sequence 200344, |
| C | 18 | -22.4 | 42.3 | 1182 | 9 | US-09-728-626-773 | A | Sequence 773, App |
| C | 19 | -22.4 | 42.3 | 1266 | 17 | US-10-781-014-619 | A | Sequence 619, App |
| C | 20 | -22.4 | 42.3 | 3309040 | 5 | US-09-738-626-1 | A | Sequence 1, App |
| C | 21 | -22.4 | 41.9 | 1880 | 15 | US-10-369-493-36410 | A | Sequence 36410, A |
| C | 22 | -22 | 41.5 | 1180 | 18 | US-10-425-115-109275 | A | Sequence 109275, |
| C | 23 | -22 | 41.5 | 1230 | 15 | US-10-021-722A-7 | A | Sequence 7, App |
| C | 24 | -22 | 41.5 | 3708 | 10 | US-09-758-036-1 | A | Sequence 1, App |
| C | 25 | -21.8 | 41.1 | 1240 | 17 | US-10-767-795-1977 | A | Sequence 1977, App |
| C | 26 | -21.8 | 41.1 | 58320 | 17 | US-10-322-281-88 | A | Sequence 88, App |
| C | 27 | -21.8 | 41.1 | 2256646 | 17 | US-10-470-565-1 | A | Sequence 1, App |
| C | 28 | -21.6 | 40.8 | 255 | 9 | US-09-923-876-1370 | A | Sequence 1370, Ap |
| C | 29 | -21.6 | 40.8 | 255 | 10 | US-09-923-876-1370 | A | Sequence 1370, Ap |
| C | 30 | -21.6 | 40.8 | 735 | 18 | US-10-653-047-7425 | A | Sequence 7425, Ap |
| C | 31 | -21.6 | 40.8 | 1071 | 16 | US-10-423-114-35778 | A | Sequence 35778, A |
| C | 32 | -21.6 | 40.8 | 1488 | 18 | US-10-818-770-55 | A | Sequence 55, App |
| C | 33 | -21.6 | 40.8 | 1554 | 16 | US-10-425-114-35214 | A | Sequence 35214, A |
| C | 34 | -21.6 | 40.8 | 1922 | 18 | US-10-425-115-9544 | A | Sequence 9544, Ap |
| C | 35 | -21.6 | 40.8 | 1554 | 18 | US-10-425-115-9553 | A | Sequence 9553, Ap |
| C | 36 | -21.6 | 40.8 | 2055 | 17 | US-10-437-963-11860 | A | Sequence 11860, A |
| C | 37 | -21.6 | 40.8 | 4800 | 15 | US-10-372-291-5 | A | Sequence 5, App |
| C | 38 | -21.6 | 40.8 | 4800 | 17 | US-10-109-048-1141 | A | Sequence 1141, Ap |
| C | 39 | -21.6 | 40.8 | 4800 | 17 | US-10-628-525-4 | A | Sequence 1630, App |
| C | 40 | -21.6 | 40.8 | 401616 | 13 | US-10-087-159-1630 | A | Sequence 145, App |
| C | 41 | -21.4 | 40.4 | 473 | 17 | US-10-437-963-145 | A | Sequence 145, App |
| C | 42 | -21.4 | 40.4 | 474 | 18 | US-10-425-115-44987 | A | Sequence 44987, A |
| C | 43 | -21.4 | 40.4 | 476 | 17 | US-10-437-963-69195 | A | Sequence 69195, A |
| C | 44 | -21.4 | 40.4 | 1309 | 16 | US-10-425-114-10976 | A | Sequence 10976, A |
| C | 45 | -21.4 | 40.4 | 1386 | 17 | US-10-767-701-13947 | A | Sequence 13947, A |

ALIGNMENTS

RESULT 1
US-10-011-033--5
Sequence 5, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSER: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
City: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber mosaic virus
STRAIN: V-34
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
OTHER INFORMATION: /codon start= 3
/function= "ENCAPSIDATES VIRUS RNA"
/product= "COAT PROTEIN"
/gene= "Cp"
/number= 1
/standard name= "COAT PROTEIN"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-011-033-5

Query Match 86.8%; Score 46; DB 13; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCATGACCAATCTGATCAACCAAGTCTGCTGTAACCGTCGACG 49
1 CCATGACCAATCTGATCAACCAAGTCTGCTGTAACCGTCGACG 46

RESULT 2

US-10-011-033-14
Sequence 14, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F

TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: A35
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-011-033-14

Query Match 86.8%; Score 46; DB 13; Length 772;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 CCATGACCAATCTGATCAACCAAGTCTGCTGTAACCGTCGACG 49
DB 1 CCATGACCAATCTGATCAACCAAGTCTGCTGTAACCGTCGACG 46

RESULT 3

US-10-011-033-3
Sequence 3, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F

TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:

ORGANISM: CUCUMBER MOSAIC VIRUS

STRAIN: v-33
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-10-011-033-3

Query Match 86.8%; Score 46; DB 13; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 CCATGACAAATCTGAATCAACCAAGTCTGTCTTAACCGTCGACG 49
1 CCATGACAAATCTGAATCAACCAAGTCTGTCTTAACCGTCGACG 46

RESULT 4

US-10-011-033-1
Sequence 1, Application US/10011033
Publication No. US20020124286A1

GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J

TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.

STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,033

FILING DATE: 13-NO. US20020124286A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/875,233

FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lisa V. Mueller

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 772 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Cucumber Mosaic Virus

INDIVIDUAL ISOLATE: V-27

FEATURE:

NAME/KEY: CDS

LOCATION: 3..660

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-011-033-1

Query Match 83.8%; Score 44.4; DB 13; Length 772;
Best Local Similarity 97.8%; Pred. No. 6.8e-08;

Matches 45; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

4 CCATGACAAATCTGAATCAACCAAGTCTGTCTTAACCGTCGACG 49
1 CCATGACAAATCTGAATCAACCAAGTCTGTCTTAACCGTCGACG 46

RESULT 5

US-10-011-033-9
Sequence 9, Application US/10011033
Publication No. US20020124286A1

GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J

TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamow & Katz, Ltd.

STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,033

FILING DATE: 13-NO. US20020124286A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/875,233

FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Lisa V. Mueller

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 960 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: CUCUMBER MOSAIC VIRUS

STRAIN: STRAIN C

FEATURE:

NAME/KEY: CDS

LOCATION: 1..658

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-011-033-9

Query Match 80.0%; Score 42.4; DB 13; Length 960;
Best Local Similarity 97.7%; Pred. No. 4.8e-07;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

6 ATGACAAATCTGAATCAACCAAGTCTGTCTTAACCGTCGACG 49
1 ATGACAAATCTGAATCAACCAAGTCTGTCTTAACCGTCGACG 44

RESULT 6

US-10-011-033-11

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      PRIOR APPLICATION DATA:
      APPLICATION NUMBER:
      FILING DATE:
      ATTORNEY/AGENT INFORMATION:
      NAME: Brookes, A. Anders
      REGISTRATION NUMBER: 36,373
      REFERENCE/DOCKET NUMBER: PB340P1
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (301) 309-8504
      TELEFAX: (301) 309-8512
      INFORMATION FOR SEQ ID NO: 373:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 1068 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: double
      TOPOLOGY: linear
      US-08-961-527-373

Query Match      45.3%; Score 24; DB 8; Length 1068;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Cy      13  AATCTGAATCAACCACTGCTGTCGTCAACCGTCGACGAGC 52
      |||||
Db      150  AATCTGATCATCAACCACTGCTGCTCACTCAGCATGACACAC 189

RESULT 8
; Sequence 373, Application US/10158844
; Publication No. US20040029118A1
GENERAL INFORMATION:
APPLICANT: Kunisch et al.
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude Pentium 3
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/158,844
FILING DATE: 03-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/961,527
FILING DATE: 1997-10-30
APPLICATION NUMBER: US 60/029,960
FILING DATE: 1996-10-31
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB340P1D1
INFORMATION FOR SEQ ID NO: 373:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 373:
;
; US-10-158-844-373

Query Match      45.3%; Score 24; DB 16; Length 1068;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy 13 AATCTGAATCAACGAGTGTGCTGTAACCGTGCAGC 52
| | | | | | | | | | | | | | | | | | | | | |
Db 150 AATCTGAATCAACGAGTGTGCTGTAACCGTGCAGC 189

RESULT 9
US-10-424-599-77125

; Sequence 77125, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 77125
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_40658C.1
US-10-424-599-77125

Query Match 44.5%; Score 23.6; DB 16; Length 352;
Best Local Similarity 76.3%; Pred. No. 19;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 13 AATCTGAATCAACGAGTGTGCTGTAACCGTGCAGC 50
| | | | | | | | | | | | | | | | | | | | | |
Db 155 AATCTGAATCAACGAGTGTGCTGTAACCGTGCAGC 192

RESULT 10
US-10-369-493-37626

; Sequence 37626, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 37626
; LENGTH: 1680
; TYPE: DNA
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-37626

Query Match 43.8%; Score 23.2; DB 15; Length 1680;
Best Local Similarity 65.4%; Pred. No. 40;
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 GATCCATGACAAATCTGAATCAACGAGTGTGCTGTAACCGTGCAGC 52
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Db 1021 GTTTCATGTGCGCATCTGAACGATGAATTGATGGCGGACGAGAGC 1072

RESULT 11
US-09-905-666A-20
; Sequence 20, Application US/09905666A

; Publication No. US20030096390A1
; GENERAL INFORMATION:
; APPLICANT: GIVER, LORRAINE J.
; APPLICANT: MINSHULL, JEREMY
; APPLICANT: VOGEL, KURT
; TITLE OF INVENTION: NOVEL LIPASE GENES
; FILE REFERENCE: 0184.310US
; CURRENT APPLICATION NUMBER: US/09/905,666A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/217,954
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/300,378
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Bacillus sp.
US-09-905-666A-20

Query Match 43.0%; Score 22.8; DB 10; Length 642;
Best Local Similarity 66.0%; Pred. No. 46;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 4 CCATGACAAATCTGAATCAACGAGTGTGCTGTAACCGTGCAGC 53
| | | | | | | | | | | | | | | | | | | | | |
Db 436 CCATGACAAATCTGAATCAACGAGTGTGCTGTAACCGTGCAGC 485

RESULT 12
US-10-437-963-47739

; Sequence 47739, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 47739
; LENGTH: 766
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_50479C.1
US-10-437-963-47739

Query Match 43.0%; Score 22.8; DB 17; Length 766;
Best Local Similarity 71.4%; Pred. No. 48;
Matches 30; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 ATCCATGACAAATCTGAATCAACGAGTGTGCTGTAACCG 43
| | | | | | | | | | | | | | | | | | | | | |
Db 300 AACCTGTCCAACTCGAGACTCTGCCAATCTGTGTGAGCG 341

RESULT 13
US-10-437-963-34792/C
; Sequence 34792, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bouharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 34792
LENGTH: 2718
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MFT4530_38773C.1
US-10-437-963-34792

Query Match 42.6%; Score 22.6; DB 17; Length 2718;
Best Local Similarity: 75.7%; Pred. No. 80;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 16 CTGAATCAACCAAGTGTGTCGTAAACCGTCGACGAGC 52
Db 519 CTGAACATGCCGCGCTGCGAGTAACCGAGACGAGC 483

RESULT 14
US-10-087-192-37/c
Sequence 37, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 122859
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(122859)
OTHER INFORMATION: n = A,T,C or G
US-10-087-192-37

Query Match 42.6%; Score 22.6; DB 13; Length 122859;
Best Local Similarity: 75.7%; Pred. No. 2.1e+02;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 ATCCATGACAAATCTGAATCAACCAAGTGTGTCGT 38
Db 9102 AGCCTTGACAAATCTTAATGAACGATGTGTGAGGT 9066

RESULT 15
US-09-939-964-1
Sequence 1, Application US/09939964
Publication No. US20030054522A1
GENERAL INFORMATION:
APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph

APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
FILE REFERENCE: CARP0068
CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 536165
TYPE: DNA
ORGANISM: Rhizobium
US-09-939-964-1

Query Match 42.6%; Score 22.6; DB 10; Length 536165;
Best Local Similarity: 68.9%; Pred. No. 3e+02;
Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 9 GACAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACGAGCT 53
Db 525007 GACGAAGTGGATCATGACGTGCTGATCGCAACGCTGACCGGCT 525051

Search completed: December 5, 2004, 07:06:42
Job time : 232 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 06:13:23 ; Search time 221 Seconds
(without alignments)
1258.911 Million cell updates/sec

Title: US-09-857-841-3
Perfect score: 53
Sequence: 1 gatccatgacgaactctgaa.....gtcgtacacgtgcagagct 53

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|-------------|
| 1 | 53 | 100.0 | 53 | AAA30858 | Ubiquitin |
| 2 | 46 | 86.8 | 771 | AAT34666 | Coat prot |
| 3 | 46 | 86.8 | 773 | AAT34665 | Coat prot |
| 4 | 45 | 84.9 | 976 | AAQ10461 | Capid pr |
| 5 | 45 | 84.9 | 1007 | AAQ10462 | Capid pr |
| 6 | 45 | 84.9 | 1007 | AAQ67395 | Caulliflow |
| 7 | 45 | 84.9 | 1066 | AAT99545 | Cucumber |
| 8 | 45 | 84.9 | 1067 | AAZ07505 | Cucumber |
| 9 | 45 | 84.9 | 1379 | AAH81111 | Sequence |
| 10 | 45 | 84.9 | 1696 | AAQ76107 | Cucumber |
| 11 | 45 | 84.9 | 1860 | AAQ76106 | Cucumber |
| 12 | 45 | 84.9 | 2173 | AAQ76108 | Cucumber |
| 13 | 43 | 81.1 | 772 | AAT34664 | Coat prot |
| 14 | 43 | 81.1 | 772 | AAT17259 | Coat prot |
| 15 | 38 | 71.7 | 894 | ABL58209 | Agrobacte |
| 16 | 38 | 71.7 | 1423 | AAH90249 | Cucumber |
| 17 | 38 | 71.7 | 1426 | AAT72272 | Cucumber |
| 18 | 37 | 69.8 | 657 | AAQ03641 | Cucumber |
| 19 | 20 | 37.7 | 25 | AAQ00796 | Primer YR |
| 20 | 17 | 32.1 | 20 | AAQ80688 | CMV-SA CD |
| 21 | 17 | 32.1 | 639 | AAA64858 | Bordetell |

| | | | | | | |
|----|----|------|--------|----|----------|------------------|
| 22 | 17 | 32.1 | 657 | 2 | AAQ41742 | Aa41742 Cucumber |
| 23 | 17 | 32.1 | 657 | 2 | AAQ80683 | CMV-SA co |
| 24 | 17 | 32.1 | 1128 | 3 | AAQ45252 | Arabidops |
| 25 | 17 | 32.1 | 1132 | 3 | AAC36474 | Arabidops |
| 26 | 17 | 32.1 | 28854 | 8 | ABX95685 | Human gen |
| 27 | 17 | 32.1 | 35026 | 3 | AAA64890 | Bordetell |
| 28 | 17 | 32.1 | 334462 | 10 | ADC24763 | Human wil |
| 29 | 16 | 30.2 | 35 | 2 | AAQ92815 | DNA prime |
| 30 | 16 | 30.2 | 542 | 4 | AAT8246 | peatis |
| 31 | 16 | 30.2 | 542 | 4 | AAQ43396 | DNA encod |
| 32 | 16 | 30.2 | 542 | 4 | AAI93810 | Human pol |
| 33 | 16 | 30.2 | 639 | 3 | AAZ45575 | Nucleotid |
| 34 | 16 | 30.2 | 762 | 4 | ABL09345 | Drosophil |
| 35 | 16 | 30.2 | 3118 | 4 | ABL09344 | Drosophil |
| 36 | 16 | 30.2 | 4116 | 6 | ABK24522 | EIF-2alph |
| 37 | 16 | 30.2 | 11463 | 2 | AAH34650 | Starch br |
| 38 | 16 | 30.2 | 11475 | 5 | AAH78338 | Nucleotid |
| 39 | 16 | 30.2 | 11476 | 12 | ADH9961 | A. tausch |
| 40 | 16 | 30.2 | 13500 | 3 | AAZ45562 | Nucleotid |
| 41 | 16 | 30.2 | 335199 | 10 | ADC24703 | Human wil |
| 42 | 15 | 28.3 | 99 | 12 | ADG93176 | Novel exp |
| 43 | 15 | 28.3 | 99 | 12 | ADG93175 | Novel exp |
| 44 | 15 | 28.3 | 99 | 12 | ADU65853 | Novel exp |
| 45 | 15 | 28.3 | 99 | 12 | ADU65854 | Novel exp |

ALIGNMENTS

| | | |
|----------|---|--|
| RESULT 1 | AAA30858 | standard; DNA; 53 BP. |
| ID | AAA30858; | |
| AC | AAA30858; | |
| DT | 19-SEP-2000 | (first entry) |
| XX | Ubiquitin monomer C-terminal fragment coding sequence. | |
| DE | Ubiquitin monomer; protein production; plant cell; ubiquitin promoter; | |
| XX | ds. | |
| KW | Nicotiana tabacum. | |
| XX | OS | |
| PH | Key | Location/Qualifiers |
| FT | CDS | 6..47 |
| FT | | /*tag= a |
| FT | | /product= "Ubiquitin_monomer_fragment" |
| FT | | /partial |
| XX | W0200036129-A1. | |
| XX | 22-JUN-2000. | |
| PD | 11-DEC-1998; | 98WO-SG000103. |
| XX | 11-DEC-1998; | 98WO-SG000103. |
| PF | (MOLE-) INST MOLECULAR AGRICULTURE. | |
| XX | Fang R, Wu J, Chen X; | |
| PI | WPI: 2000-433604/37. | |
| XX | P-PSDB; AAY90255. | |
| DR | Production of desired protein in plants or plant cells by linking a | |
| XX | ubiquitin monomer coding sequence upstream of the gene encoding the | |
| PT | desired protein. | |
| XX | Claim 8, Page 18, 42pp; English. | |
| PS | This sequence encodes the C-terminal fragment of a ubiquitin monomer. The | |
| XX | invention relates to a method for enhancing production of a desired | |
| CC | | |

CC protein in a plant or plant cell by inserting a nucleic acid (NA)
CC encoding a ubiquitin monomer upstream of a NA encoding the desired
CC protein, where the fusion construct encodes a fusion protein and
CC expression is not controlled by the ubiquitin promoter. The invention
CC also relates to a NA acid vector a NA vector able to transform a plant
CC cell, that comprises NA encoding a fusion protein having a ubiquitin
CC monomer linked to a protein of interest and further, where expression of
CC the fusion construct is not under control of a ubiquitin promoter. The
CC construct allows enhanced production of the desired protein in plants or
CC plant cells

XX Sequence 53 BP; 15 A; 14 C; 13 G; 11 T; 0 U; 0 Other;

SO Query Match 100.0%; Score 53; DB 3; Length 53;

Best Local Similarity 100.0%; Pred. No. 6.1e-13;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GATCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACGAGCT 53
1 CATTGATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACGAGCT 53

RESULT 2
AAT34666

ID AAT34666 standard; DNA; 771 BP.

AC AAT34666;

DT 16-OCT-2003 (revised)
02-DEC-1996 (first entry)

DE Coat protein of the V34 strain of cucumber mosaic virus.

KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
resistance; ss.

OS Cucumber mosaic virus; strain V34.

XX Key Location/Qualifiers

FT CDS 3..659

FT CDS /*tag= a

XX MO9621018-A1.

XX 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

XX WPI; 1996-333993/33.

XX P-PSDB; AAR98895.

XX New isolated cucumber mosaic virus coat protein DNA - used to produce

XX plant, partic. of the family Cucurbitaceae or Solanaceae, which are

XX resistant to infection.

XX Claim 24; Fig 3; 80pp; English.

XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber

XX mosaic virus (CMV) were isolated. The CMV CP genes were isolated from

XX infected plant tissue by PCR amplification of cDNA using primers based on

XX known CP sequences. The genes may be used for producing plants such as

XX quash, cucumber, peppers and tomatoes which are resistant to CMV

XX infection. (Updated on 16-OCT-2003 to standardise OS field)

SO Sequence 771 BP; 176 A; 199 C; 183 G; 213 T; 0 U; 0 Other;

Query Match 86.8%; Score 46; DB 2; Length 771;

Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 CCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 49
1 CATTGATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 46

RESULT 3
AAT34665

ID AAT34665 standard; DNA; 773 BP.

AC AAT34665;

DT 16-OCT-2003 (revised)
02-DEC-1996 (first entry)

DE Coat protein of the V33 strain of cucumber mosaic virus.

KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
resistance; ss.

OS Cucumber mosaic virus; strain V33.

XX Key Location/Qualifiers

FT CDS 3..659

FT CDS /*tag= a

XX MO9621018-A1.

XX 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

XX WPI; 1996-333993/33.

XX P-PSDB; AAR98894.

XX New isolated cucumber mosaic virus coat protein DNA - used to produce

XX plant, partic. of the family Cucurbitaceae or Solanaceae, which are

XX resistant to infection.

XX Claim 13; Fig 2; 80pp; English.

XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber

XX mosaic virus (CMV) were isolated. The CMV CP genes were isolated from

XX infected plant tissue by PCR amplification of cDNA using primers based on

XX known CP sequences. The genes may be used for producing plants such as

XX quash, cucumber, peppers and tomatoes which are resistant to CMV

XX infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 773 BP; 175 A; 200 C; 185 G; 213 T; 0 U; 0 Other;

Query Match 86.8%; Score 46; DB 2; Length 773;

Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 CCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 49
1 CATTGATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 46

RESULT 4
AAQ10461

ID AAQ10461 standard; cDNA; 976 BP.

AC AAQ10461;


```
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-APR-1991 (first entry)
XX Capsid protein gene of Cucumber Mosaic Virus strain FNY.
XX
XX CMV; resistance; capsid protein; Cucumis melo; ss.
XX
XX Cucumber mosaic virus.
XX
XX Key Location/Qualifiers
XX CDS 75..731
XX /*tag= a
XX /product= "CMV strain FNY capsid protein"
XX
XX EP412912-A.
XX
XX 13-FEB-1991.
XX
XX 09-AUG-1990; 90EP-00402282.
XX
XX 11-AUG-1989; 89FR-00010848.
XX
XX (BIOC-) BIOCEM SA.
XX
XX Deboth M, Bentahar S, Noel M, Perret J;
XX
XX WPI; 1991-046027/07.
XX
XX P-PSDB; AAR10652.
XX
XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
XX culture on specific medium for new transformed plants etc., esp.
XX resistant to cucumber mosaic virus.
XX
XX Claim 15; Page 17; 44pp; French.
XX
XX The gene was isolated from a plasmid (pUC18) containing DNA complementary
XX to RNA 3 of the virulent strain FNY, isolated in New York on infected
XX melons. The sequence includes a leader sequence, coding region and 3' non
XX -coding region. The leader sequence is the same length as that of the
XX Japanese Y strain of CMV. Transgenic melon plantlets containing the
XX sequence introduced via an Agrobacterium tumefaciens intermediate are
XX cultured as shoots in special media. The transformed melon plants are
XX resistant to CMV. See also AA010462. (Updated on 25-MAR-2003 to correct
XX PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX AUG-2003 to correct OS field.)
XX
XX Sequence 976 BP; 224 A; 249 C; 230 G; 273 T; 0 U; 0 Other;
SQ
Query Match 84.9%; Score 45; DB 2; Length 976;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 74 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 118
RESULT 5
AA010462
ID AA010462 standard; DNA; 1007 BP.
XX
XX AA010462;
XX
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 16-APR-1991 (first entry)
XX
XX Capsid protein gene of Cucumber Mosaic Virus strain 117F.
XX
XX CMV; resistance; capsid protein; Cucumis melo; ss.
XX
XX Cucumber mosaic virus.
OS
```

```
XX
XX Key Location/Qualifiers
XX CDS 54..710
XX /*tag= a
XX /product= "CMV strain 117F capsid protein"
XX
XX EP412912-A.
XX
XX 13-FEB-1991.
XX
XX 09-AUG-1990; 90EP-00402282.
XX
XX 11-AUG-1989; 89FR-00010848.
XX
XX (BIOC-) BIOCEM SA.
XX
XX Deboth M, Bentahar S, Noel M, Perret J;
XX
XX WPI; 1991-046027/07.
XX
XX P-PSDB; AAR10653.
XX
XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
XX culture on specific medium for new transformed plants etc., esp.
XX resistant to cucumber mosaic virus.
XX
XX Claim 16; Page 19; 44pp; French.
XX
XX The gene was isolated from the virulent French strain 117F of CMV. Tomato
XX plantlets at the 2-leaf stage were infected with CMV strain 117F. 15 days
XX post-infection, the virus was purified from the infected leaves and cDNA
XX was synthesised from RNAs 1,2,3 and 4. After purification and selection
XX by standard techniques, cDNA complementary to RNA 4 was found to encode
XX the capsid protein. It was recloned into "blue scribe" plasmids and
XX sequenced. Transgenic melon plantlets containing the sequence introduced
XX via an Agrobacterium tumefaciens intermediate are cultured as shoots in
XX special media. The transformed melon plants are resistant to CMV. See
XX also AA010461. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
XX 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
XX field.)
XX
XX Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;
SQ
Query Match 84.9%; Score 45; DB 2; Length 1007;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 49
DB 53 CATGACAAATCTGAATCAACCAAGTGTGCTGTAACCGTCGACG 97
RESULT 6
AA067395
ID AA067395 standard; DNA; 1007 BP.
XX
XX AA067395;
XX
XX 25-MAR-2003 (revised)
XX 12-APR-1995 (first entry)
XX
XX Cauliflower mosaic virus capsid protein coding sequence.
XX
XX Cauliflower mosaic virus; CMV; capsid protein; coat protein;
XX polyribozyme; inactivator; inactivation; resistance; crop protection; ss.
XX
XX Cauliflower mosaic virus.
XX
XX Key Location/Qualifiers
XX CDS 54..710
XX /*tag= a
XX /product= "Capsid protein."
XX
XX FR2701960-A1.
```

```
XX 02-SEP-1994.
PD 93FR-00002269.
XX 26-FEB-1993; 93FR-00002269.
XX 26-FEB-1993; 93FR-00002269.
XX (GENE-) GENE SHEARS PTY LTD.
XX
XX Lenee P, Perez P, Gruber V, Baudot G, Ollivo C;
XX WPI; 1994-281767/35.
XX P-PSDB; AAR57968.
XX
XX New polyribozyme contg. several catalytic regions in complementary
XX sequence - can inactivate gene for viral capsid protein, esp. for prepn.
XX of new virus resistant transgenic plants, also DNA sequence encoding it.
XX
XX Disclosure; Fig 2; 67pp; French.
XX
XX The RNA encoding the capsid protein of cauliflower mosaic virus can be
XX targeted by a nucleic acid sequence called a "polyribozyme". The
XX polyribozyme has endoribonuclease activity and is able to inactivate the
XX gene encoding the viral capsid protein. The polyribozyme comprises
XX several catalytic regions derived from ribozymes and confers complete
XX resistance to virus. See AA067391-94. (Updated on 25-MAR-2003 to correct
XX PN field.)
XX
XX Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;
SQ
Query Match 84.9%; Score 45; DB 2; Length 1007;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CATGACAAATCTGATCAACGAGTGTGTCGTAAACGTCGACG 49
DB 53 CATGACAAATCTGATCAACGAGTGTGTCGTAAACGTCGACG 97
RESULT 7
ID AAT99545/c
AC AAT99545;
XX 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
XX Cucurbit mosaic virus RNA-3 cDNA fragment.
DE
XX Transgenic plant; virus resistance; disease resistance; RNA virus; CMV;
XX coat protein; antisense gene; ss.
XX
XX Cucurbit mosaic virus.
OS
XX
XX Key Location/Qualifiers
XX 3'UTR 1..299
XX CDS 300..958
XX /tag= a
XX /product= "coat protein"
XX /tag= b
XX /product= "coat protein"
XX /tag= c
XX /note= "Coat protein leader sequence"
XX /tag= d
XX /note= "F sequence of sub-genomic promoter"
XX
XX EP806481-A2.
XX 12-NOV-1997.
XX
XX 07-MAY-1997; 97EP-00201379.
```

```
XX 09-MAY-1996; 96IT-MI000927.
XX (META-) METAPONTUM AGROBIOS SCRL.
XX
XX Cellini F, Grieco PD;
XX WPI; 1997-538620/50.
XX
XX Preparing transgenic plants resistant to RNA virus infection - using
XX anti-sense gene constructs containing the viral coat protein gene, e.g.
XX from cucumber mosaic virus.
XX
XX Claim 3; Page 10; 18pp; English.
XX
XX This cDNA clone of cucumber mosaic virus (CMV) RNA-3 includes domain F of
XX the subgenomic promoter of viral RNA, the coat protein gene, its leader
XX sequence, and the RNA-3-like 3'-terminal region of RNA-3. It was prepared
XX by amplifying a fragment of CMV cDNA-3 from clone PCR-CMV1RNA3 by PCR
XX (see also AAT99548-49). The gene construct is introduced into a vector
XX containing a promoter active in plant cells in antisense orientation
XX relative to the promoter. A claimed recombinant vector comprises the
XX plant promoter, the antisense gene construct and a terminator which is
XX functional in the plant. In addition to CMV, viral RNA may also be used
XX from tobacco mosaic virus and potato virus. Claimed transgenic plants
XX have the antisense gene construct integrated into their genomes. They are
XX resistant to viral infection. In particular, they are resistant to CMV.
XX Within the antisense gene construct, the interfering activity of the
XX antisense F domain of the sub-genomic promoter, associated with the
XX antisense activity performed by the coat protein gene, allows production
XX of plants having 100% resistance to CMV. (Updated on 25-MAR-2003 to
XX correct PR field.)
XX
XX Sequence 1066 BP; 299 A; 251 C; 273 G; 243 T; 0 U; 0 Other;
SQ
Query Match 84.9%; Score 45; DB 2; Length 1066;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CATGACAAATCTGATCAACGAGTGTGTCGTAAACGTCGACG 49
DB 957 CATGACAAATCTGATCAACGAGTGTGTCGTAAACGTCGACG 913
RESULT 8
ID AA207505/c
AC AA207505;
XX 26-NOV-1999 (first entry)
DT
XX
XX Cucurbit mosaic virus (CMV) RNA-3 gene cDNA clone fragment.
DE
XX
XX Transgenic plant; RNA virus; antisense construct; cucumber mosaic virus;
XX CMV; promoter; coat protein gene; infection; RNA-3; ss.
XX
XX Cucurbit mosaic virus.
OS
XX
XX US959181-A.
XX 28-SEP-1999.
XX
XX 09-MAY-1997; 97US-00854170.
XX 09-MAY-1996; 96IT-MI000927.
XX
XX (META-) METAPONTUM AGROBIOS SCRL.
XX Cellini F, Grieco PD;
XX WPI; 1997-538620/50.
XX
```

PT Preparing transgenic plants resistant to RNA virus infection - using
PT anti-sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
PS Claim 2; Fig 1; 15pp; English.
XX
CC The invention relates to preparing transgenic plants resistant to RNA
CC virus induced infections that comprises integrating an antisense gene
CC construct into the plant genome. The construct comprises: (a) an F domain
CC of a subgenomic promoter of cucumber mosaic virus (CMV); (b) downstream
CC from the subgenomic promoter, a leader sequence of a coat protein gene of
CC CMV; (c) downstream from the leader sequence, a gene encoding a CMV coat
CC protein; and (d) downstream from the gene, a 3'-terminal region of a CMV
CC coat protein gene. The method is useful for producing plants which are
CC resistant to infection by RNA based viruses. The gene construct gives
CC higher levels of resistance compared to antisense constructs which are
CC capable of complementing with different domains of genomic RNA of CMV.
CC The present sequence represents the fragment of cDNA clone of RNA-3 of
CC CMV. This forms the antisense construct of the invention
XX
SQ Sequence 1067 BP; 297 A; 250 C; 276 G; 244 T; 0 U; 0 Other;
Query Match 84.9%; Score 45; DB 2; Length 1067;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CATGACAAATCTGATCAACAGCTGCTGCTAACCGTCGACG 49
DB 957 CATGACAAATCTGATCAACAGCTGCTGCTAACCGTCGACG 913
RESULT 9
ID AAN81111 standard; DNA; 1379 BP.
AC AAN81111;
XX
XX 25-MAR-2003 (revised)
DT 12-NOV-1990 (first entry)
XX
DE Sequence contg. CMV strain Y coat protein gene.
XX
KW Cucumber mosaic virus; plant viral resistance; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 418..1074
FT /*tag= a
FT /label= cucumber mosaic virus-Y coat protein.
XX
FN EP279433-A.
XX
PD 24-AUG-1988.
XX
PF 18-FEB-1988; 88EP-00102322.
XX
PR 20-FEB-1987; 87JP-00038288.
PR 25-FEB-1987; 87JP-00043443.
PR 18-FEB-1988; 88JP-00035809.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Furusawa I, Onda H, Komiya T;
XX
DR WPI; 1988-236708/34.
DR P-PSDB; AAP80509.
XX
PT DNA coding for the coat protein of cucumber mosaic virus strain Y - used
PT for producing plants resistant to cucumber mosaic virus infection.
PS Disclosure; Page ?; 20pp; English.
XX

CC This DNA is produced on screening of a plasmid library and is used to
CC transform plant cells which subsequently produce the coat prot- ein of
CC cucumber mosaic virus (CMV) strain Y. This protein is not synthesised in
CC natural plant cells. The resistance to CMV infect- ion, provided by the
CC DNA, is shown in plant cells and redifferent- iated plant bodies. See
CC also AAN81110. (Updated on 25-MAR-2003 to correct PR field.) (Updated on
CC 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1379 BP; 306 A; 342 C; 333 G; 398 T; 0 U; 0 Other;
Query Match 84.9%; Score 45; DB 1; Length 1379;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CATGACAAATCTGATCAACAGCTGCTGCTAACCGTCGACG 49
DB 417 CATGACAAATCTGATCAACAGCTGCTGCTAACCGTCGACG 461
RESULT 10
ID AAQ76107 standard; DNA; 1696 BP.
AC AAQ76107;
XX
XX 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE Cucumber mosaic virus RNA-3 chimera encoding RNase TI.
XX
KW Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; RNase TI;
KW cell inhibitory protein; TOMV; CMV; ss.
XX
OS Cucumber mosaic virus.
XX
FH Key Location/Qualifiers
FT CDS 123..437
FT /*tag= a
FT /product= "RNase TI"
XX
FN M09429464-A1.
XX
PD 22-DEC-1994.
XX
PF 03-JUN-1994; 94WO-EP001817.
XX
PR 04-JUN-1993; 93GB-00011593.
XX
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI De Haan PT;
XX
DR WPI; 1995-036490/05.
DR P-PSDB; AAR67754.
XX
PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.
XX
PS Claim 4; Page 31-32; 50pp; English.
XX
XX A chimeric cucumber mosaic virus RNA-3 (given in AAQ76107) has the coat
XX protein gene replaced by a gene encoding a cell inhibitory protein, RNase
XX TI, having the sequence given in AAR67754. The construct elicits a minus-
XX sense RNA that interacts with the RNA-dependent RNA-polymerase of an
XX invading virus, thus conferring virus-resistance on a host plant, e.g.
XX tobacco, tomato. (Updated on 25-MAR-2003 to correct PN field.)
XX

SO Sequence 1696 BP; 387 A; 413 C; 389 G; 507 T; 0 U; 0 Other;
Query Match 84.9%; Score 45; DB 2; Length 1696;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CATGACAAATCTGAATCAACCACTGCTGCTGAACCGTCGACG 49
DB 732 CATGACAAATCTGAATCAACCACTGCTGCTGAACCGTCGACG 776
RESULT 11
AAQ76106
ID AAQ76106 standard; DNA; 1860 BP.
XX AAQ76106;
AC
XX 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
XX Cucurbit mosaic virus RNA-3 chimera encoding TOMV CP.
DE
XX Cucurbit mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; coat protein; CP;
KW TOMV; CMV; ss.
XX
XX Cucurbit mosaic virus.
OS
XX
XX Key Location/Qualifiers
FH 123. .600
FT /tag= a
FT /product= "TOMV coat protein"
FT CDS 895. .1550
FT /tag= b
FT /product= "CMV coat protein"
XX
XX WO9429464-A1.
PN
XX 22-DEC-1994.
PD
XX 03-JUN-1994; 94WO-EP001817.
PF
XX 04-JUN-1993; 93GB-00011593.
PR
XX
XX (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
XX De Haan PT;
PI
XX
XX WPI; 1995-036490/05.
DR P-PSDB; AAR67752, AAR67753.
XX
XX DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.
XX
XX Claim 3; Page 27-28; 50pp; English.
XX
XX A chimeric cucumber mosaic virus RNA-3 (given in AAQ76106) codes for the
CC coat protein (CP) of tomato mosaic virus (AAR67752) as well as its own CP
CC (AAR67753). The construct elicits minus-sense RNA that interacts with the
CC RNA-dependent RNA-polymerase of an invading virus, thus conferring virus-
CC resistance on a host plant, e.g. tobacco, tomato. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
XX Sequence 1860 BP; 448 A; 429 C; 431 G; 552 T; 0 U; 0 Other;
SO
Query Match 84.9%; Score 45; DB 2; Length 1860;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CATGACAAATCTGAATCAACCACTGCTGCTGAACCGTCGACG 49
DB 896 CATGACAAATCTGAATCAACCACTGCTGCTGAACCGTCGACG 940
RESULT 12
AAQ76108
ID AAQ76108 standard; DNA; 2173 BP.
XX AAQ76108;
AC
XX 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
XX Cucurbit mosaic virus RNA-3 chimera encoding TOMV P30.
DE
XX Cucurbit mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; P30; elicitor; TOMV;
KW CMV; ss.
XX
XX Cucurbit mosaic virus.
OS
XX
XX Key Location/Qualifiers
FH 123. .914
FT /tag= a
FT /product= "TOMV P30 elicitor"
FT CDS
FT
XX
XX WO9429464-A1.
PN
XX 22-DEC-1994.
PD
XX 03-JUN-1994; 94WO-EP001817.
PF
XX 04-JUN-1993; 93GB-00011593.
PR
XX
XX (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
XX De Haan PT;
PI
XX
XX WPI; 1995-036490/05.
DR P-PSDB; AAR67755.
XX
XX DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.
XX
XX Claim 5; Page 34-35; 50pp; English.
XX
XX A chimeric cucumber mosaic virus RNA-3 (given in AAQ76108) has the coat
CC protein gene replaced by a gene encoding an elicitor, TOMV P30, having
CC the sequence given in AAR67755. The construct elicits a minus-sense RNA
CC that interacts with the RNA-dependent RNA-polymerase of an invading
CC virus, thus conferring virus-resistance on a host plant, e.g. tobacco,
CC tomato. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 2173 BP; 561 A; 438 C; 532 G; 642 T; 0 U; 0 Other;
SO
Query Match 84.9%; Score 45; DB 2; Length 2173;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CATGACAAATCTGAATCAACCACTGCTGCTGAACCGTCGACG 49
DB 1209 CATGACAAATCTGAATCAACCACTGCTGCTGAACCGTCGACG 1253
RESULT 13
AAT34664

```
ID AAT34664 standard; DNA; 772 BP.
XX
AC AAT34664;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the V27 strain of cucumber mosaic virus.
XX
KM Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
XX resistance; ss.
XX
OS Cucumber mosaic virus; strain V27.
XX
FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a
XX
PN MO9621018-A1.
XX
PD 11-JUL-1996.
XX
PE 07-JUN-1995; 95WO-US007234.
XX
PR 30-DEC-1994; 94US-00367789.
XX
PA (ASGR-) ASGROW SEED CO.
XX
PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX WPI; 1996-333993/33.
XX DR P-PSDB; AAR98893.
XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
PS Claim 2; Fig 1; 80pp; English.
XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 772 BP; 177 A; 202 C; 182 G; 211 T; 0 U; 0 Other;
XX
Query Match 81.1%; Score 43; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4 CCATGACAAATCTGAATCAACCACTGCTGCTGCTAACCGTCG 46
DB 1 CCATGACAAATCTGAATCAACCACTGCTGCTGCTAACCGTCG 43
XX
RESULT 14
AAT17259
ID AAT17259 standard; DNA; 772 BP.
XX
AC AAT17259;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the A35 strain of cucumber mosaic virus.
XX
KM Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
XX resistance; ss.
XX
OS Cucumber mosaic virus; strain A35.
XX
```

```
FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a
XX
PN MO9621018-A1.
XX
PD 11-JUL-1996.
XX
PE 07-JUN-1995; 95WO-US007234.
XX
PR 30-DEC-1994; 94US-00367789.
XX
PA (ASGR-) ASGROW SEED CO.
XX
PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX WPI; 1996-333993/33.
XX DR P-PSDB; AAR93803.
XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
PS Disclosure; Fig 8; 80pp; English.
XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 772 BP; 175 A; 201 C; 185 G; 211 T; 0 U; 0 Other;
XX
Query Match 81.1%; Score 43; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4 CCATGACAAATCTGAATCAACCACTGCTGCTGCTAACCGTCG 46
DB 1 CCATGACAAATCTGAATCAACCACTGCTGCTGCTAACCGTCG 43
XX
RESULT 15
ABL58209
ID ABL58209 standard; DNA; 894 BP.
XX
AC ABL58209;
XX
DT 25-JUL-2002 (first entry)
XX
DE Agrobacterium tumefaciens coding sequence.
XX
KM Agrobacterium tumefaciens; anti-cucumber mosaic virus; transgenic tomato;
XX ss.
XX
OS Agrobacterium tumefaciens.
XX
FH Key Location/Qualifiers
FT CDS 105..760
FT /*tag= a
FT /product= "Agrobacterium tumefaciens protein"
XX
PN KR99075101-A.
XX
PD 05-OCT-1999.
XX
PE 17-MAR-1998; 98KR-00009096.
XX
PR 17-MAR-1998; 98KR-00009096.
XX
PA (RURA-) RURAL DEV ADMINISTRATION.
XX
```

PI Sohn SH, Lee SW, Park JS, Hwang YS;
 XX
 DR MPI; 2000-577926/54.
 DR P-PSDB; ABB80503.
 XX
 FT Anti-cucumber mosaic virus tomato.
 XX
 PS Disclosure; Page 4; 6pp; Korean.
 XX
 CC This sequence represents a coding sequence from Agrobacterium tumefaciens
 CC used within the scope of the invention. The invention relates to an anti-
 CC cucumber mosaic virus tomato
 XX
 SQ Sequence 894 BP; 188 A; 228 C; 216 G; 262 T; 0 U; 0 Other;
 Query Match 71.7%; Score 38; DB 3; Length 894;
 Best Local Similarity 100.0%; Pred. No. 7.6e-11; Indels 0; Gaps 0;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 AAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 49
 |||||
 DB 111 AAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 148

Search completed: December 5, 2004, 07:10:27
 Job time : 223 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2004, 07:10:32 ; Search time 71 Seconds
(without alignments)
70.735 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSGAGNR 14

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 69 | 100.0 | 14 | 3 | AA90255 Ubiquitin |
| 2 | 69 | 100.0 | 218 | 2 | AA10652 Capsid pr |
| 3 | 69 | 100.0 | 218 | 2 | AA10653 Capsid pr |
| 4 | 69 | 100.0 | 218 | 2 | AA57968 Cauliflow |
| 5 | 69 | 100.0 | 218 | 2 | AA67753 CMV coat |
| 6 | 69 | 100.0 | 218 | 2 | AA93803 Coat prot |
| 7 | 69 | 100.0 | 218 | 2 | AA98893 Coat prot |
| 8 | 69 | 100.0 | 218 | 2 | AA98894 Coat prot |
| 9 | 69 | 100.0 | 218 | 2 | AA98895 Coat prot |
| 10 | 69 | 100.0 | 218 | 2 | AA98895 Coat prot |
| 11 | 44 | 63.8 | 438 | 8 | AB880503 |
| 12 | 42 | 60.9 | 218 | 2 | AA37212 Cucumbe |
| 13 | 40 | 58.0 | 289 | 3 | AA605253 Arabidops |
| 14 | 39 | 56.5 | 64 | 8 | ABO57865 Human sec |
| 15 | 39 | 56.5 | 64 | 8 | ABO57865 Human gen |
| 16 | 39 | 56.5 | 261 | 6 | AAE36184 Human CGD |
| 17 | 39 | 56.5 | 271 | 4 | AA41266 Human pol |
| 18 | 39 | 56.5 | 274 | 4 | AAU23534 Novel hum |
| 19 | 39 | 56.5 | 280 | 6 | ABU11773 Human MDD |
| 20 | 39 | 56.5 | 287 | 4 | AA39480 Human pol |
| 21 | 39 | 56.5 | 407 | 4 | AB61652 Drosophi |
| 22 | 39 | 56.5 | 1046 | 7 | AD58906 Human pro |
| 23 | 39 | 56.5 | 1046 | 7 | AD45534 Human pro |
| 24 | 39 | 56.5 | 1046 | 7 | AD61258 Human pro |
| 25 | 39 | 56.5 | 1046 | 7 | AD58902 Human pro |

| | | | | | | |
|----|----|------|-------|---|----------|--------------------|
| 26 | 38 | 55.1 | 54 | 4 | AAU41552 | AAU41552 Propionib |
| 27 | 38 | 55.1 | 54 | 6 | ABM38071 | ABM38071 Propionib |
| 28 | 38 | 55.1 | 197 | 8 | AD057439 | AD057439 Hairless |
| 29 | 38 | 55.1 | 372 | 2 | AA22239 | AA22239 Human ZP3 |
| 30 | 38 | 55.1 | 372 | 2 | AA67287 | AA67287 Human zon |
| 31 | 38 | 55.1 | 530 | 7 | ADCO7876 | ADCO7876 Rice prot |
| 32 | 38 | 55.1 | 530 | 7 | ADCO8287 | ADCO8287 Rice prot |
| 33 | 38 | 55.1 | 562 | 8 | ADP43232 | ADP43232 Nematode |
| 34 | 38 | 55.1 | 624 | 8 | ADP43243 | ADP43243 Nematode |
| 35 | 38 | 55.1 | 626 | 8 | ADP43242 | ADP43242 Nematode |
| 36 | 38 | 55.1 | 1511 | 2 | AA132080 | AA132080 Yeast wea |
| 37 | 38 | 55.1 | 1517 | 3 | AA38482 | AA38482 Arabidops |
| 38 | 38 | 55.1 | 1543 | 3 | AA38481 | AA38481 Arabidops |
| 39 | 38 | 55.1 | 1672 | 3 | AA38480 | AA38480 Arabidops |
| 40 | 38 | 55.1 | 19938 | 6 | ABP76680 | ABP76680 Streptomy |
| 41 | 37 | 53.6 | 69 | 5 | ABP03145 | ABP03145 Human ORF |
| 42 | 37 | 53.6 | 86 | 3 | AA62614 | AA62614 Arabidops |
| 43 | 37 | 53.6 | 95 | 4 | AAU66349 | AAU66349 Propionib |
| 44 | 37 | 53.6 | 95 | 4 | AAU66349 | AAU66349 Propionib |
| 45 | 37 | 53.6 | 95 | 6 | ABM61147 | ABM61147 Propionib |

ALIGNMENTS

| | | |
|----------|--|---------------------------|
| RESULT 1 | AA90255 | standard; protein; 14 AA. |
| ID | AA90255 | |
| XX | AA90255; | |
| XX | AC | |
| XX | 19-SEP-2000 (first entry) | |
| DT | XX | |
| XX | Ubiquitin monomer C-terminal fragment. | |
| DB | XX | |
| XX | Ubiquitin monomer; protein production; plant cell; ubiquitin promoter. | |
| KW | XX | |
| XX | Nicotiana tabacum. | |
| OS | XX | |
| XX | MO200036129-A1. | |
| PN | XX | |
| PD | XX | |
| XX | 22-JUN-2000. | |
| XX | PF | |
| XX | 11-DEC-1998; 98WO-SG000103. | |
| XX | PR | |
| XX | 11-DEC-1998; 98WO-SG000103. | |
| XX | PA | |
| XX | (MOLE-) INST MOLECULAR AGROBIOLOGY. | |
| XX | Fang R, Wu J, Chen X; | |
| PI | XX | |
| XX | WPI; 2000-431604/37. | |
| DR | XX | |
| XX | N-PSDB; AAA30858. | |
| XX | PT | |
| PT | production of desired protein in plants or plant cells by linking a | |
| PT | ubiquitin monomer coding sequence upstream of the gene encoding the | |
| PT | desired protein. | |
| XX | XX | |
| PS | Claim 7; Page 18; 42pp; English. | |
| XX | XX | |
| CC | This sequence represents the C-terminal fragment of a ubiquitin monomer. | |
| CC | The invention relates to a method for enhancing production of a desired | |
| CC | protein in a plant or plant cell by inserting a nucleic acid (NA) | |
| CC | encoding a ubiquitin monomer upstream of a NA encoding the desired | |
| CC | protein, where the fusion construct encodes a fusion protein and | |
| CC | expression is not controlled by the ubiquitin promoter. The invention | |
| CC | also relates to a NA encoding a fusion protein having a ubiquitin | |
| CC | cell, that comprises NA encoding a fusion protein having a ubiquitin | |
| CC | monomer linked to a protein of interest and further, where expression of | |
| CC | the fusion construct is not under control of a ubiquitin promoter. The | |
| CC | construct allows enhanced production of the desired protein in plants or | |
| CC | plant cells | |

SQ Sequence 14 AA;

Query Match 100.0%; Score 69; DB 3; Length 14;

Best Local Similarity 100.0%; Pred. No. 3.8e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14

1 MDKSESTAGRNRR 14

DB 1 MDKSESTAGRNRR 14

RESULT 2

AAR10652 standard; protein; 218 AA.

XX AAR10652;

XX 27-AUG-2003 (revised)

XX 25-MAR-2003 (revised)

XX 16-APR-1991 (first entry)

XX Capsid protein of Cucumber Mosaic Virus strain FNY.

XX CMV; resistance; capsid protein; Cucumis melo.

XX Cucurbit mosaic virus.

XX EP412912-A.

XX 13-FEB-1991.

XX 09-AUG-1990; 90EP-00402282.

XX 11-AUG-1989; 89FR-00010848.

XX (BIOC-) BIOCEM SA.

XX Deboth M, Bentahar S, Noel M, Perret J;

XX WPI; 1991-046027/07.

XX N-PSDB; AAQ10461.

XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage

XX PT culture on specific medium for new transformed plants etc., esp.

XX PT resistant to cucumber mosaic virus.

XX Claim 15; Page 17; 44pp; French.

XX The gene encoding this protein was isolated from a plasmid (pUC18)

XX containing DNA complementary to RNA 3 of the virulent strain FNY,

XX isolated in New York on infected melons. Transgenic melon plantlets

XX containing the nucleotide sequence introduced via an Agrobacterium

XX tumefaciens intermediate are cultured as shoots in special media. The

XX transformed melon plants are resistant to CMV. See also AAQ10462.

XX (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to

XX correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 218 AA;

XX Query Match 100.0%; Score 69; DB 2; Length 218;

XX Best Local Similarity 100.0%; Pred. No. 0.00071;

XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14

1 MDKSESTAGRNRR 14

DB 1 MDKSESTAGRNRR 14

RESULT 3

AAR10653 standard; protein; 218 AA.

XX AAR10653;

XX 27-AUG-2003 (revised)

XX 25-MAR-2003 (revised)

XX 16-APR-1991 (first entry)

XX Capsid protein of Cucumber Mosaic Virus strain 117F.

XX CMV; strain 117F; resistance; capsid protein; Cucumis melo.

XX Cucurbit mosaic virus.

XX EP412912-A.

XX 13-FEB-1991.

XX 09-AUG-1990; 90EP-00402282.

XX 11-AUG-1989; 89FR-00010848.

XX (BIOC-) BIOCEM SA.

XX Deboth M, Bentahar S, Noel M, Perret J;

XX WPI; 1991-046027/07.

XX N-PSDB; AAQ10462.

XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage

XX PT culture on specific medium for new transformed plants etc., esp.

XX PT resistant to cucumber mosaic virus.

XX Claim 16; Page 19; 44pp; French.

XX The gene encoding this protein was isolated from the virulent French

XX strain 117F of CMV. Transgenic melon plantlets containing the coding

XX sequence (introduced via an Agrobacterium tumefaciens intermediate) are

XX cultured as shoots in special media. The transformed melon plants are

XX resistant to CMV. See also AAQ10461. (Updated on 25-MAR-2003 to correct

XX PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-

XX AUG-2003 to correct OS field.)

XX Sequence 218 AA;

XX Query Match 100.0%; Score 69; DB 2; Length 218;

XX Best Local Similarity 100.0%; Pred. No. 0.00071;

XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14

1 MDKSESTAGRNRR 14

DB 1 MDKSESTAGRNRR 14

RESULT 4

AAR57968 standard; protein; 218 AA.

XX AAR57968;

XX 25-MAR-2003 (revised)

XX 20-APR-1995 (first entry)

XX Cauliflower mosaic virus capsid protein.

XX Cauliflower mosaic virus; CMV; capsid protein; coat protein;

XX polyribosyme; inactivate; inactivation; resistance; crop protection.

XX Cauliflower mosaic virus.

XX FR2701960-A1.

XX 02-SEP-1994.

XX 26-FEB-1993; 93FR-00002269.

PR 26-FEB-1993; 93FR-00002269.
XX (GENE-) GENE SHEARS PTY LTD.
PA Lenae P, Perez P, Gruber V, Baudot G, Ollivo C;
XX WPI; 1994-281767/35.
DR N-PSDB; AAQ67395.
XX
PT New polyribozyme contg. several catalytic regions in complementary
PT sequence - can inactivate gene for viral capsid protein, esp. for prepn.
PT of new virus resistant transgenic plants, also DNA sequence encoding it.
XX
PS Disclosure; Fig 2; 67pp; French.
XX The RNA encoding the capsid protein of cauliflower mosaic virus can be
CC targeted by a nucleic acid sequence called a "polyribozyme". The
CC polyribozyme has endoribonuclease activity and is able to inactivate the
CC gene encoding the viral capsid protein. The polyribozyme comprises
CC several catalytic regions derived from ribozymes and confers complete
CC resistance to virus. See AAQ67391-94. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 218 AA;
XX
Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071; Mismatches 0; Gaps 0;
Matches 14; Conservative 0; Indels 0;
OY 1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14
XX
RESULT 5
AAR67753
ID AAR67753 standard; protein; 218 AA.
XX
AC AAR67753;
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE CMV coat protein.
XX
KW Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KW virus resistance; disease resistance; transgenic plant; cross protection;
KW hypersensitive response; crop improvement; tomato;
KW Lycopersicon esculentum; tobacco; Nicotiana tabacum; coat protein; CP;
KW TMV; CMV.
XX
OS Cucumber mosaic virus.
XX
PN MO9429464-A1.
XX
PD 22-DEC-1994.
XX
PF 03-JUN-1994; 94WO-EP001817.
XX
PR 04-JUN-1993; 93GB-00011593.
XX
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI De Haan PT;
XX
DR WPI; 1995-036490/05.
DR N-PSDB; AAQ76106.
XX
PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.

XX
PS Disclosure; Page 30; 50pp; English.
XX
CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76106) codes for the
CC coat protein (CP) of tomato mosaic virus (AAR67552) as well as its own CP
CC (AAR67753). The construct elicits minus-sense RNA that interacts with the
CC RNA-dependent RNA-polymerase of an invading virus, thus conferring virus-
CC resistance on a host plant, e.g. tobacco, tomato. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 218 AA;
XX
Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071; Mismatches 0; Gaps 0;
Matches 14; Conservative 0; Indels 0;
OY 1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14
XX
RESULT 6
AAR93803
ID AAR93803 standard; protein; 218 AA.
XX
AC AAR93803;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the A35 strain of cucumber mosaic virus.
XX
KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KW resistance.
XX
OS Cucumber mosaic virus; strain A35.
XX
PN MO9621018-A1.
XX
PD 11-JUL-1996.
XX
PF 07-JUN-1995; 95WO-US007234.
XX
PR 30-DEC-1994; 94US-00367789.
XX
PA (ASGR-) ASGROW SEED CO.
XX
PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
DR WPI; 1996-333993/33.
DR N-PSDB; AAT17259.
XX
PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
PS Disclosure; Fig 8; 80pp; English.
XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 218 AA;
XX
Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071; Mismatches 0; Gaps 0;
Matches 14; Conservative 0; Indels 0;
OY 1 MDKSESTSGRNR 14

Db 1 MDKSESTSGRNR 14

RESULT 7
AAR98893
ID AAR98893 standard; protein; 218 AA.
XX
XX AAR98893;
AC
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the V27 strain of cucumber mosaic virus.
XX
XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance.
XX
XX Cucumber mosaic virus; strain V27.
XX
XX WO9621018-A1.
XX
XX 11-JUL-1996.
XX
XX 07-JUN-1995; 95WO-US007234.
XX
XX 30-DEC-1994; 94US-00367789.
XX
XX (ASGR-) ASGROW SEED CO.
XX
XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
XX WPI; 1996-333993/33.
XX
XX N-PSDB; AAT34664.
XX
XX New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
XX
XX Disclosure; Fig 1; 80pp; English.
XX
XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGRNR 14
Db 1 MDKSESTSGRNR 14

RESULT 8
AAR98894
ID AAR98894 standard; protein; 218 AA.
XX
XX AAR98894;
AC
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the V33 strain of cucumber mosaic virus.
XX
XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance.
XX
XX Cucumber mosaic virus; strain V33.
OS

XX
XX WO9621018-A1.
XX
XX 11-JUL-1996.
XX
XX 07-JUN-1995; 95WO-US007234.
XX
XX 30-DEC-1994; 94US-00367789.
XX
XX (ASGR-) ASGROW SEED CO.
XX
XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
XX WPI; 1996-333993/33.
XX
XX N-PSDB; AAT34665.
XX
XX New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
XX
XX Disclosure; Fig 2; 80pp; English.
XX
XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGRNR 14
Db 1 MDKSESTSGRNR 14

RESULT 9
AAR98895
ID AAR98895 standard; protein; 218 AA.
XX
XX AAR98895;
AC
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
XX
XX Coat protein of the V34 strain of cucumber mosaic virus.
XX
XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance.
XX
XX Cucumber mosaic virus; strain V34.
XX
XX WO9621018-A1.
XX
XX 11-JUL-1996.
XX
XX 07-JUN-1995; 95WO-US007234.
XX
XX 30-DEC-1994; 94US-00367789.
XX
XX (ASGR-) ASGROW SEED CO.
XX
XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
XX WPI; 1996-333993/33.
XX
XX N-PSDB; AAT34666.
XX
XX New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.

PT resistant to infection.
XX
XX
PS Disclosure; Fig 3; 80pp; English.
XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC squash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 218 AA;
Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKSESTSGRRNR 14
DB 1 MDKSESTSGRRNR 14
RESULT 10
ID ABB80503 standard; protein; 218 AA.
XX
AC ABB80503;
XX
DT 25-JUL-2002 (first entry)
XX
DE Agrobacterium tumefaciens protein sequence.
XX
XX Agrobacterium tumefaciens; anti-cucumber mosaic virus; transgenic tomato.
XX OS Agrobacterium tumefaciens.
XX PN KR9075101-A.
XX
PD 05-OCT-1999.
XX
PF 17-MAR-1998; 98KR-00009096.
XX
PR 17-MAR-1998; 98KR-00009096.
XX
PA (RURA-) RURAL DEV ADMINISTRATION.
XX
XX Sohn SH, Lee SW, Park JS, Hwang YS;
XX WPI: 2000-577926/54.
XX DR N-PSDB; ABL58209.
XX
PT Anti-cucumber mosaic virus tomato.
XX
PS Disclosure; Page 4; 6pp; Korean.
XX
CC This sequence represents a protein sequence from Agrobacterium
CC tumefaciens used within the scope of the invention. The invention relates
CC to an anti-cucumber mosaic virus tomato
XX
SQ Sequence 218 AA;
Query Match 88.4%; Score 61; DB 3; Length 218;
Best Local Similarity 92.9%; Pred. No. 0.018;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDKSESTSGRRNR 14
DB 1 MDKSESTSGRRNR 14
RESULT 11
ID ADO61973
ADO61973 standard; protein; 438 AA.

XX
AC ADO61973;
XX
DT 15-JUL-2004 (first entry)
XX
DE Transcription factor G2565, SEQ ID 440.
XX
XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;
XX osmotic stress tolerance; cold tolerance; heat tolerance;
XX low nitrogen tolerance; low phosphate tolerance; fungal diseases;
XX glyphosate resistance; flowering; fertility; seed development.
XX
XX Arabidopsis thaliana.
XX
XX WO2004031349-A2.
XX
PD 15-APR-2004.
XX
PF 18-SEP-2003; 2003MO-US030292.
XX
PR 18-SEP-2002; 2002US-0411837P.
PR 17-DEC-2002; 2002US-0434166P.
PR 24-APR-2003; 2003US-0465809P.
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
PI Jiang C, Heard JB, Ratcliffe O, Creelman RA, Adam LJ, Reuber TL;
PI Riechmann JL, Haake V, Dubell AN, Keddie JS, Sherman BK;
XX
XX WPI: 2004-330163/30.
XX
XX N-PSDB; ADO61972.
XX
PT New recombinant polynucleotide encoding transcription factor
PT polypeptides, useful for producing transgenic plants with advantageous
PT properties compared to a reference plant.
XX
XX
PS Disclosure; SEQ ID NO 440; 510pp; English.
XX
XX The present invention relates to novel plant transcription factor
XX proteins (I) and nucleotide sequences (II) (ADO61534-ADO63778). The
XX sequences can be used to produce transgenic plants, which overexpress
XX (II), where the transgenic plant has an altered trait as compared to a
XX non-transgenic plant or wild-type plant. The transgenic plant comprises
XX an altered trait selected from increased tolerance to abiotic stress,
XX increased tolerance to osmotic stress, increased tolerance to cold,
XX increased germination in cold, increased tolerance to heat, increased
XX germination in heat, increased tolerance to freezing conditions,
XX increased tolerance to low nitrogen conditions, increased tolerance to
XX low phosphate conditions, increased tolerance to disease, including
XX fungal disease and particularly Erysiphe, Fusarium and Botrytis,
XX increased tolerance to multiple fungal pathogens, increased resistance to
XX glyphosate, increased sensitivity to ABA, reduced sensitivity to ABA,
XX increased sensitivity to ACC, altered sugar sensing, increased tolerance
XX to sugars, altered carbon/nitrogen sensing, early flowering, late
XX flowering, altered flower structure, loss of flower determinacy, reduced
XX fertility, altered shoot meristem development, altered branching pattern,
XX altered stem morphology, altered vascular tissue structure, reduced
XX apical dominance, altered trichome density, altered trichome development,
XX altered trichome structure, altered root development, altered shade
XX avoidance, altered seed development, altered seed ripening, altered seed
XX germination, slow growth, fast growth, altered cell differentiation,
XX altered cell proliferation, altered cell expansion, altered phase change,
XX altered senescence, abnormal embryo development, altered programmed cell
XX death, lethality when overexpressed, altered necrosis patterns, increased
XX plant size, increased biomass, large seedlings, dwarfed plants, dark
XX green leaves, change in leaf shape, increased leaf size and mass, light
XX green or gray leaves, glossy leaves, altered abaxial/adaxial polarity,
XX altered seed coloration, altered seed size, altered seed shape, large
XX seed, increased leaf wax, increased leaf fatty acids, altered seed oil
XX content, altered seed protein content, altered seedprenyl content,
XX altered leaf prenyl lipid content, increased anthocyanin levels, and
XX decreased anthocyanin levels. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in

| | | |
|----|-------------|----------------|
| PR | 18-JUN-1999 | 99US-01394566P |
| PR | 18-JUN-1999 | 99US-01394587P |
| PR | 18-JUN-1999 | 99US-01394588P |
| PR | 18-JUN-1999 | 99US-01394599P |
| PR | 18-JUN-1999 | 99US-01394609P |
| PR | 18-JUN-1999 | 99US-01394610P |
| PR | 18-JUN-1999 | 99US-01394612P |
| PR | 18-JUN-1999 | 99US-01394636P |
| PR | 18-JUN-1999 | 99US-01397500P |
| PR | 18-JUN-1999 | 99US-01397630P |
| PR | 21-JUN-1999 | 99US-01398177P |
| PR | 22-JUN-1999 | 99US-01398699P |
| PR | 23-JUN-1999 | 99US-0140353P |
| PR | 23-JUN-1999 | 99US-0140354P |
| PR | 02-JUL-1999 | 99US-0142055P |
| PR | 06-JUL-1999 | 99US-0142390P |
| PR | 08-JUL-1999 | 99US-0142803P |
| PR | 09-JUL-1999 | 99US-0142820P |
| PR | 12-JUL-1999 | 99US-0142877P |
| PR | 13-JUL-1999 | 99US-0143542P |
| PR | 14-JUL-1999 | 99US-0143624P |
| PR | 15-JUL-1999 | 99US-0144005P |
| PR | 16-JUL-1999 | 99US-0144085P |
| PR | 16-JUL-1999 | 99US-0144086P |
| PR | 19-JUL-1999 | 99US-0144331P |
| PR | 19-JUL-1999 | 99US-0144332P |
| PR | 19-JUL-1999 | 99US-0144333P |
| PR | 19-JUL-1999 | 99US-0144334P |
| PR | 20-JUL-1999 | 99US-0144335P |
| PR | 20-JUL-1999 | 99US-0144352P |
| PR | 20-JUL-1999 | 99US-0144632P |
| PR | 20-JUL-1999 | 99US-0144684P |
| PR | 21-JUL-1999 | 99US-0144814P |
| PR | 21-JUL-1999 | 99US-0145086P |
| PR | 21-JUL-1999 | 99US-0145088P |
| PR | 21-JUL-1999 | 99US-0145087P |
| PR | 22-JUL-1999 | 99US-0145089P |
| PR | 22-JUL-1999 | 99US-0145192P |
| PR | 22-JUL-1999 | 99US-0145145P |
| PR | 22-JUL-1999 | 99US-0145224P |
| PR | 23-JUL-1999 | 99US-0145218P |
| PR | 23-JUL-1999 | 99US-0145249P |
| PR | 26-JUL-1999 | 99US-0145766P |
| PR | 26-JUL-1999 | 99US-0145913P |
| PR | 27-JUL-1999 | 99US-0145918P |
| PR | 27-JUL-1999 | 99US-0145919P |
| PR | 28-JUL-1999 | 99US-0145951P |
| PR | 02-AUG-1999 | 99US-0146388P |
| PR | 02-AUG-1999 | 99US-0146389P |
| PR | 02-AUG-1999 | 99US-0146398P |
| PR | 03-AUG-1999 | 99US-0147038P |
| PR | 04-AUG-1999 | 99US-0147204P |
| PR | 04-AUG-1999 | 99US-0147302P |
| PR | 05-AUG-1999 | 99US-0147192P |
| PR | 11-AUG-1999 | 99US-0148171P |
| PR | 12-AUG-1999 | 99US-0148319P |
| PR | 13-AUG-1999 | 99US-0148341P |
| PR | 13-AUG-1999 | 99US-0148565P |
| PR | 17-AUG-1999 | 99US-0148684P |
| PR | 17-AUG-1999 | 99US-0149368P |
| PR | 17-AUG-1999 | 99US-0149175P |

| | | |
|----|-------------|---------------|
| PR | 28-AUG-1999 | 99US-0149426P |
| PR | 20-AUG-1999 | 99US-0149723P |
| PR | 20-AUG-1999 | 99US-0149723P |
| PR | 20-AUG-1999 | 99US-0149932P |
| PR | 23-AUG-1999 | 99US-0149902P |
| PR | 23-AUG-1999 | 99US-0149930P |
| PR | 25-AUG-1999 | 99US-0149930P |
| PR | 26-AUG-1999 | 99US-0150884P |
| PR | 27-AUG-1999 | 99US-0151065P |
| PR | 27-AUG-1999 | 99US-0151066P |
| PR | 30-AUG-1999 | 99US-0151080P |
| PR | 31-AUG-1999 | 99US-0151303P |
| PR | 01-SEP-1999 | 99US-0151438P |
| PR | 07-SEP-1999 | 99US-0152633P |
| PR | 10-SEP-1999 | 99US-0153070P |
| PR | 13-SEP-1999 | 99US-0153758P |
| PR | 15-SEP-1999 | 99US-0154031P |
| PR | 16-SEP-1999 | 99US-0154039P |
| PR | 20-SEP-1999 | 99US-0155477P |
| PR | 22-SEP-1999 | 99US-0155413P |
| PR | 23-SEP-1999 | 99US-0155486P |
| PR | 24-SEP-1999 | 99US-0155659P |
| PR | 28-SEP-1999 | 99US-0156458P |
| PR | 29-SEP-1999 | 99US-0156569P |
| PR | 04-OCT-1999 | 99US-0157117P |
| PR | 05-OCT-1999 | 99US-0157753P |
| PR | 06-OCT-1999 | 99US-0157865P |
| PR | 07-OCT-1999 | 99US-0158029P |
| PR | 08-OCT-1999 | 99US-0158932P |
| PR | 12-OCT-1999 | 99US-0158369P |
| PR | 13-OCT-1999 | 99US-0159293P |
| PR | 13-OCT-1999 | 99US-0159294P |
| PR | 13-OCT-1999 | 99US-0159294P |
| PR | 13-OCT-1999 | 99US-0159295P |
| PR | 14-OCT-1999 | 99US-0159320P |
| PR | 14-OCT-1999 | 99US-0159331P |
| PR | 14-OCT-1999 | 99US-0159637P |
| PR | 14-OCT-1999 | 99US-0159638P |
| PR | 18-OCT-1999 | 99US-0159584P |
| PR | 21-OCT-1999 | 99US-0160741P |
| PR | 21-OCT-1999 | 99US-0160767P |
| PR | 21-OCT-1999 | 99US-0160768P |
| PR | 21-OCT-1999 | 99US-0160770P |
| PR | 21-OCT-1999 | 99US-0160814P |
| PR | 21-OCT-1999 | 99US-0160815P |
| PR | 22-OCT-1999 | 99US-0160980P |
| PR | 22-OCT-1999 | 99US-0160981P |
| PR | 22-OCT-1999 | 99US-0160989P |
| PR | 25-OCT-1999 | 99US-0161404P |
| PR | 25-OCT-1999 | 99US-0161405P |
| PR | 25-OCT-1999 | 99US-0161406P |
| PR | 26-OCT-1999 | 99US-0161539P |
| PR | 26-OCT-1999 | 99US-0161560P |
| PR | 26-OCT-1999 | 99US-0161613P |
| PR | 28-OCT-1999 | 99US-0161932P |
| PR | 28-OCT-1999 | 99US-0161939P |
| PR | 29-OCT-1999 | 99US-0162142P |

| | | | | |
|-----------------------|--------|--------------------|--------|---------------|
| Query Match | 58.0%; | Score 40; | DB 3; | Length 289; |
| Best Local Similarity | 72.7%; | Pred. No. 1.2e+02; | | |
| Matches | 8; | Conservative | 1; | Mismatches 2; |
| | | | Indels | 0; |
| | | | Gaps | 0; |

| | | | | | |
|----|----|--------|------|---|----|
| QY | 2 | DKSEST | SAGR | N | 12 |
| | | | | | |
| | | | : | | |
| Db | 17 | DSSSSS | SAGR | N | 27 |

RESULT 14
AAG00746
ID AAG00746 standard; protein; 64 AA.
XX

AC AAG00746;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 4827.
XX
KW Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KM gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
DR N-PSDB; AAC00752.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 13; SEQ ID NO 4827; 71pp + Sequence Listing; English.
XX
CC The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors
XX
XX Sequence 64 AA;
SQ
Query Match 56.5%; Score 39; DB 3; Length 64;
Best Local Similarity 58.3%; Pred. No. 36;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 3 KSESTSGRNR 14
:||||:|:|:
DB 53 QSESTNGKNKR 64
RESULT 15
AB057865
ID AB057865 standard; protein; 68 AA.
XX
XX AB057865;
AC
DT 29-JUL-2004 (first entry)
XX
XX Human genome derived single exon protein #4099.
DE
XX
XX Human; gene expression; single exon probe; microarray;
KM alternative splicing event; genomic alteration.
XX
XX Homo sapiens.
OS
XX
XX US2003194704-A1.
PY

XX
PD 16-OCT-2003.
XX
XX
PR 03-APR-2002; 2002US-00029386.
XX
XX
PR 03-APR-2002; 2002US-00029386.
XX
XX
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
P1 Penn SG, Rank DR, Hanzel DK;
XX
XX WPI; 2004-119264/12.
DR
XX
PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
XX
PS Claim 45; SEQ ID NO 31499; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and
XX encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX fully defined in the specification. The probe is a single exon probe that
XX hybridizes under high stringency conditions to a nucleic acid molecule
XX expressed in human cells or tissues. Also included are a spatially-
XX addressable set of single exon nucleic acid probes for measuring human
XX gene expression (comprising a plurality of single exon nucleic acid
XX probes cited above, where each of the plurality of probes is separately
XX and addressably isolatable or amplifiable from the plurality), a single
XX exon microarray for measuring human gene expression, a method of
XX measuring human gene expression, a vector comprising the single exon
XX probe cited above, an ORF-encoded peptide comprising at least 8
XX contiguous amino acids of any of the above-mentioned amino acid
XX sequences (optionally with conservative amino acid substitutions), an
XX isolated antibody that binds specifically to a peptide cited above,
XX methods of selling and/or licensing single exon probes or microarrays to
XX a customer desiring to measure gene expression, a method of providing
XX human gene expression data by subcription, and a computer-readable
XX storage medium which contains a database having a plurality of records
XX (each record including data on the expression of a single exon probe
XX cited above. The probe, methods and apparatus are useful in gene
XX expression analysis. The probes may be used as tools for surveying
XX tissues to detect the presence of expressed messages that contain their
XX specific exon, or in constructing genome-derived single exon microarrays.
XX In addition, the probes are used in identifying and characterizing
XX alternative splicing events, in detecting and characterizing gross
XX alterations in the genomic locus that includes their exon, in assessing
XX smaller genomic alterations, in printing the synthesis of nucleic acids,
XX or in expressing the ORF-encoded peptide. The present sequence is a human
XX single exon probe protein of the invention. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?docid=20030194704
XX
SQ Sequence 68 AA;
Query Match 56.5%; Score 39; DB 8; Length 68;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 3 KSESTSGRNR 14
:||||:|:|:
DB 31 QSESTNGKNKR 42

Search completed: December 5, 2004, 08:05:23
Job time : 74 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2004, 07:34:22 ; Search time 23 Seconds
(without alignments)
58.567 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSGRNR 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: PIR.79:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 69 | 100.0 | 218 | 1 | UQ1253 |
| 2 | 69 | 100.0 | 218 | 1 | UQ1254 |
| 3 | 69 | 100.0 | 218 | 1 | UQ1255 |
| 4 | 69 | 100.0 | 218 | 1 | UQ1256 |
| 5 | 69 | 100.0 | 218 | 1 | UQ1257 |
| 6 | 69 | 100.0 | 218 | 2 | SA2098 |
| 7 | 69 | 100.0 | 218 | 2 | SA2099 |
| 8 | 69 | 100.0 | 218 | 2 | SA2100 |
| 9 | 69 | 100.0 | 218 | 2 | SA2101 |
| 10 | 69 | 100.0 | 218 | 2 | SA2102 |
| 11 | 69 | 100.0 | 218 | 2 | SA2103 |
| 12 | 69 | 100.0 | 218 | 2 | SA2104 |
| 13 | 69 | 100.0 | 218 | 2 | SA2105 |
| 14 | 69 | 100.0 | 218 | 2 | SA2106 |
| 15 | 69 | 100.0 | 218 | 2 | SA2107 |
| 16 | 69 | 100.0 | 218 | 2 | SA2108 |
| 17 | 69 | 100.0 | 218 | 2 | SA2109 |
| 18 | 69 | 100.0 | 218 | 2 | SA2110 |
| 19 | 69 | 100.0 | 218 | 2 | SA2111 |
| 20 | 69 | 100.0 | 218 | 2 | SA2112 |
| 21 | 69 | 100.0 | 218 | 2 | SA2113 |
| 22 | 69 | 100.0 | 218 | 2 | SA2114 |
| 23 | 69 | 100.0 | 218 | 2 | SA2115 |
| 24 | 69 | 100.0 | 218 | 2 | SA2116 |
| 25 | 69 | 100.0 | 218 | 2 | SA2117 |
| 26 | 69 | 100.0 | 218 | 2 | SA2118 |
| 27 | 69 | 100.0 | 218 | 2 | SA2119 |
| 28 | 69 | 100.0 | 218 | 2 | SA2120 |
| 29 | 69 | 100.0 | 218 | 2 | SA2121 |

| | | | | | | |
|----|----|------|------|---|--------|--------------------|
| 30 | 36 | 52.2 | 432 | 2 | D86937 | probable membrane |
| 31 | 36 | 52.2 | 497 | 2 | C82025 | probable periplasm |
| 32 | 36 | 52.2 | 671 | 2 | C96546 | probable GTP-bind |
| 33 | 36 | 52.2 | 758 | 2 | E81217 | organic solvent to |
| 34 | 36 | 52.2 | 779 | 2 | T34390 | hypothetical prote |
| 35 | 36 | 52.2 | 802 | 2 | B81794 | hypothetical prote |
| 36 | 36 | 52.2 | 1532 | 2 | A61262 | collagen alpha 1(X |
| 37 | 36 | 52.2 | 1908 | 2 | A86311 | protein P113.14 (i |
| 38 | 36 | 51.4 | 1194 | 1 | DJBR28 | DNA-directed DNA p |
| 39 | 35 | 50.7 | 111 | 2 | A87525 | ER hand domain pro |
| 40 | 35 | 50.7 | 177 | 2 | F72715 | hypothetical prote |
| 41 | 35 | 50.7 | 218 | 1 | B46111 | coat protein - cuc |
| 42 | 35 | 50.7 | 218 | 1 | VCVXUV | coat protein - cuc |
| 43 | 35 | 50.7 | 218 | 1 | VCVXWL | coat protein - cuc |
| 44 | 35 | 50.7 | 248 | 1 | T04758 | hypothetical prote |
| 45 | 35 | 50.7 | 330 | 2 | F72209 | hypothetical prote |

ALIGNMENTS

RESULT 1
UQ1253
coat protein - cucumber mosaic virus (strain FC)
C:Species: cucumber mosaic virus, CMV
C:Date: 31-Mar-1992 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C:Accession: J01253
R:Shintaku, M.
U: Gen. Virol. 72, 2587-2589, 1991
A:Title: Coat protein gene sequences of two cucumber mosaic virus strains reveal a single
A:Reference number: J01253; MUID:92013983; PMID:1919534
A:Accession: J01253
A:Molecule type: genomic RNA
A:Residues: 1-218 <SHI>
A:Cross-references: UNIPROT:Q00259; GB:D10544; NID:g222024; PIDN:BA01403.1; PID:g222025
R:Tsunaawa, S.; Narita, K.
U: Biochem. 92, 607-613, 1982
A:Title: Micro-identification of amino-terminal acetyl amino acids in proteins.
A:Reference number: A61297; MUID:93056735; PMID:6754709
A:Contents: annotation; acetylation
C:Comment: This cucumber mosaic virus strain induces a yellow chlorosis.
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein
P:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14

RESULT 2
UQ1254
coat protein - cucumber mosaic virus (strain P6)
C:Species: cucumber mosaic virus, CMV
C:Date: 31-Mar-1992 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C:Accession: J01254
R:Shintaku, M.
U: Gen. Virol. 72, 2587-2589, 1991
A:Title: Coat protein gene sequences of two cucumber mosaic virus strains reveal a single
A:Reference number: J01253; MUID:92013983; PMID:1919534
A:Accession: J01254
A:Molecule type: genomic RNA
A:Residues: 1-218 <SHI>
A:Cross-references: UNIPROT:Q00261; GB:D10545; NID:g222026; PIDN:BA01404.1; PID:g222027
R:Tsunaawa, S.; Narita, K.
U: Biochem. 92, 607-613, 1982
A:Title: Micro-identification of amino-terminal acetyl amino acids in proteins.

A:Reference number: A61297; MUID:83056735; PMID:6754709
A:Contents: annotation; acetylation
C:Comment: This cucumber mosaic virus strain induces a yellow chlorosis.
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14
|||
Db 1 MDKSESTAGRNRR 14

RESULT 3
JS0090
coat protein - cucumber mosaic virus (strain O)
C:Species: cucumber mosaic virus, CMV
C:Date: 31-Mar-1992 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C:Accession: JS0090; PS0314
R:Hayakawa, T.; Mizukami, M.; Nakajima, M.; Suzuki, M.
J. Gen. Virol. 70, 499-504, 1989
A:Title: Complete nucleotide sequence of RNA 3 from cucumber mosaic virus (CMV) strain C
A:Reference number: JS0089; MUID:89279231; PMID:2732698
A:Accession: JS0090
A:Molecule type: mRNA
A:Residues: 1-218 <HAY>
A:Cross-references: UNIPROT:P16489; GB:D00385; NID:g222030; PID:BAA00297.1; PID:g222032
A:Accession: PS0314
A:Molecule type: protein
A:Residues: 216-218 <HA2>
R:Tsunasawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A:Title: Micro-identification of amino-terminal acetylamino acids in proteins.
A:Reference number: A61297; MUID:83056735; PMID:6754709
A:Contents: annotation; acetylation
C:Genetics:
A:Map position: segment 3
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14
|||
Db 1 MDKSESTAGRNRR 14

RESULT 4
VCVXY1
coat protein - cucumber mosaic virus (strain Y)
C:Species: cucumber mosaic virus, CMV
A:Note: host Nicotiana tabacum cv. Xanthi nc (tobacco)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: JA0097
R:Nitita, N.; Masuta, C.; Kuwata, S.; Takanami, Y.
Ann. Phytopathol. Soc. Jpn. 54, 516-522, 1989
A:Title: Comparative studies on the nucleotide sequence of cucumber mosaic virus RNA3
A:Reference number: JA0096
A:Accession: JA0097
A:Molecule type: mRNA
A:Residues: 1-218 <NIT>
A:Cross-references: UNIPROT:P18027
R:Tsunasawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A:Title: Micro-identification of amino-terminal acetylamino acids in proteins.
A:Reference number: A61297; MUID:83056735; PMID:6754709
A:Contents: annotation; acetylation

C:Comment: The genome consists of three single-stranded, positive RNAs, designated RNA1,
C:Genetics:
A:Map position: segment RNA3
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14
|||
Db 1 MDKSESTAGRNRR 14

RESULT 5
JC6075
coat protein - cucumber mosaic virus (strain CS)
C:Species: cucumber mosaic virus, CMV
C:Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C:Accession: JC6075
R:Huang, L.; Hu, J.S.; Barry, K.; Hweichung, F.
Chinese J. Virol. 12, 235-242, 1996
A:Title: Coat protein gene sequence analysis of three cucumber mosaic virus strains infect
A:Reference number: JC6073
A:Accession: JC6075
A:Molecule type: mRNA
A:Residues: 1-218 <HNA>
A:Cross-references: UNIPROT:Q8JFPX; UNIPROT:Q9DJX2; UNIPROT:Q9LPE5; UNIPROT:Q9DX3; UNIP
ROT:Q8JFPX; UNIPROT:Q9DJW5; UNIPROT:Q9LPP6; UNIPROT:Q9JFY4; UNIPROT:Q8JFPX4; UNIPROT:Q9D
6132; UNIPROT:Q9YVS2; UNIPROT:Q8JFPW8; UNIPROT:Q9ENS6; UNIPROT:Q83259; UNIPROT:Q9DWM2; UN
A:Experimental source: strain CS
A:Note: the authors translated the codon CCG for residue 83 as Gly
C:Genetics:
A:Gene: cp
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: coat protein

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14
|||
Db 1 MDKSESTAGRNRR 14

RESULT 6
S42098
coat protein - cucumber mosaic virus
C:Species: cucumber mosaic virus, CMV
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S42098
R:Hyon, S.; Park, Y.I.
submitted to the EMBL Data Library, February 1994
A:Description: Nucleotide sequence of cDNA from RNA4 of cucumber mosaic virus-A6 the Kore
A:Reference number: S42098
A:Accession: S42098
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-218 <HYO>
A:Cross-references: UNIPROT:Q66154; EMBL:X77855; NID:g457166; PID:CAA54846.1; PID:g45716
C:Superfamily: cucumber mosaic virus coat protein

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14
|||
Db 1 MDKSESTAGRNRR 14


```
RESULT 7
558039
capsid protein - cucumber mosaic virus
C/Species: cucumber mosaic virus, CMV
C/Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S58039
R/Hag, O.M.R.
submitted to the EMBL Data Library, July 1995
A/Reference number: S58039
A/Accession: S58039
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-218 <HAG>
A/Cross-references: UNIPROT:Q66157, EMBL:X89652, NID:g902619, PIDD:CAA61802.1, PID:g9026
C/Superfamily: cucumber mosaic virus coat protein

Query Match
Best Local Similarity 100.0%; Score 69; DB 2; Length 218;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 MDKSESTSGAGNRR 14
|||||
1 MDKSESTSGAGNRR 14

Db
1 MDKSESTSGAGNRR 14

RESULT 8
JC6074
coat protein - cucumber mosaic virus (strain MM)
C/Species: cucumber mosaic virus, CMV
C/Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C/Accession: JC6074
R/Huang, L.; Hu, J.S.; Barry, K.; Hweichung, F.
A/Title: Coat protein gene sequence analysis of three cucumber mosaic virus strains infe
A/Reference number: JC6073
A/Accession: JC6074
A/Molecule type: mRNA
A/Residues: 1-218 <HUA>
A/Cross-references: UNIPROT:Q83257, UNIPROT:Q55251, UNIPROT:Q9WAB3, UNIPROT:Q9YJR9, UNIF
A/Experimental source: strain MM
A/Note: the authors translated the codon CGT for residue 30 as Ala
C/Genetics:
A/Gene: cp
C/Superfamily: cucumber mosaic virus coat protein
C/Keywords: coat protein

Query Match
Best Local Similarity 100.0%; Score 69; DB 2; Length 218;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 MDKSESTSGAGNRR 14
|||||
1 MDKSESTSGAGNRR 14

Db
1 MDKSESTSGAGNRR 14

RESULT 9
JC6073
coat protein - cucumber mosaic virus (strain BS)
C/Species: cucumber mosaic virus, CMV
C/Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C/Accession: JC6073
R/Huang, L.; Hu, J.S.; Barry, K.; Hweichung, F.
A/Title: Coat protein gene sequence analysis of three cucumber mosaic virus strains infe
A/Reference number: JC6073
A/Accession: JC6073
A/Molecule type: mRNA
A/Residues: 1-218 <HUA>
A/Cross-references: UNIPROT:Q9DJW8, UNIPROT:Q9YJR7, UNIPROT:Q8JPK1, UNIPROT:Q9E2V6, UNIF
PROT:Q91PP6, UNIPROT:Q9JFY4, UNIPROT:Q66157, UNIPROT:Q66130, UNIPROT:Q8JPK4, UNIPROT:Q9D
6132, UNIPROT:Q9YJS2, UNIPROT:Q8JPM8, UNIPROT:Q9ENS6, UNIPROT:Q83259, UNIPROT:Q9DJW2, UN
A/Experimental source: strain BS
```

```
A/Note: the authors translated the codon CCA for residue 56 as Thr and CCC for residue 15.
C/Genetics:
A/Gene: cp
C/Superfamily: cucumber mosaic virus coat protein
C/Keywords: coat protein

Query Match
Best Local Similarity 100.0%; Score 69; DB 2; Length 218;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 MDKSESTSGAGNRR 14
|||||
1 MDKSESTSGAGNRR 14

Db
1 MDKSESTSGAGNRR 14

RESULT 10
S09663
coat protein - cucumber mosaic virus (strain I17F)
C/Species: cucumber mosaic virus, CMV
A/Variety: strain I17F
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S09663; S06932
R/Noel, M.J.T.; Tahar, S.B.
A/Title: Corrigendum. Nucleotide sequence of the coat protein gene and flanking regions
A/Reference number: S09663; MUID:90206832; PMID:2320436
A/Accession: S09663
A/Molecule type: mRNA
A/Residues: 1-218 <NOE>
A/Cross-references: UNIPROT:P14767
A/Experimental source: strain I17F
A/Note: this is a revision to the sequence from reference S06932
R/Noel, M.J.T.; Tahar, S.B.
A/Title: Nucleotide sequence of the coat protein gene and flanking regions of Cucumber M
A/Reference number: S06932; MUID:90098885; PMID:2602158
A/Accession: S06932
A/Molecule type: mRNA
A/Residues: 1-6,'W',8-44,'W',46-51,'W',53-56,'W',58-68,'W',70,'W',72-73,'W',75-96,'W',98-
A/Cross-references: EMBL:X16386
A/Experimental source: strain I17F
A/Note: this sequence has been revised in reference S09663
C/Superfamily: cucumber mosaic virus coat protein

Query Match
Best Local Similarity 100.0%; Score 69; DB 2; Length 218;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 MDKSESTSGAGNRR 14
|||||
1 MDKSESTSGAGNRR 14

Db
1 MDKSESTSGAGNRR 14

RESULT 11
JA0136
coat protein - cucumber mosaic virus (strain C)
C/Species: cucumber mosaic virus, CMV
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: JA0136
R/Quemada, H.; Kearney, C.; Gonzalez, D.; Slightom, J.L.
J. Gen. Virol. 70, 1065-1073, 1989
A/Title: Nucleotide sequences of the coat protein genes and flanking regions of cucumber
A/Reference number: JU0087; MUID:89279284; PMID:2732712
A/Accession: JA0136
A/Molecule type: genomic RNA
A/Residues: 1-218 <QBE>
A/Cross-references: UNIPROT:P21368; GB:D00462; NID:g222041; PIDD:BAA00357.1; PID:g222042
R/Tanaka, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A/Title: Micro-identification of amino-terminal acetyl amino acids in proteins.
A/Reference number: A61297; MUID:83056735; PMID:6754709
A/Contents: annotation; acetylation
C/Genetics:
```

A:Map position: segment RNA3
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein; glycoprotein
F:1/Modified site: acetylated amino end (Met) #status experimental
F:43/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.8%; Score 64; DB 1; Length 218;
Best Local Similarity 92.9%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDKSESTSGAGRRR 14
DB 1 MDKSESTSGAGRRR 14

RESULT 12
D71392
coat protein - cucumber mosaic virus (strain Ixora)
N:Alternate names: capsid protein
C:Species: cucumber mosaic virus, CMV
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C:Accession: D71392
R:McGarvey, P.; Tounsiqant, M.; Geletka, L.; Cellini, F.; Kaper, J.M.
J. Gen. Virol. 76, 2257-2270, 1995
A:Title: The complete sequence of a cucumber mosaic virus from Ixora that is deficient in
A:Reference number: A71392; MUID:96005047; PMID:7561763
A:Accession: D71392
A:Molecule type: mRNA
A:Residues: 1-218 <MCG>
A:Cross-references: UNIPROT:Q66120; GB:U20219; NID:G161916; PIDN:AAC54619.1; PID:G11619
A:Experimental source: strain Ixora
C:Comment: The CMV genome consists of three species of single-stranded, capped, positive
A:Genetics: The Ixora strain in unusual in that it does not replicate several well charac
ptons found when replicated by other CMV strains.

A:Map position: segment RNA 3
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein
F:1/Modified site: acetylated amino end (Met) #status predicted

Query Match 92.8%; Score 64; DB 2; Length 218;
Best Local Similarity 92.9%; Pred. No. 0.0003;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDKSESTSGAGRRR 14
DB 1 MDKSESTSGAGRRR 14

RESULT 13
T21432
hypochemical protein F26H11.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21432
R:Barlow, K.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19421
A:Accession: T21432
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1711 <WIL>
A:Cross-references: UNIPROT:O45409; EMBL:Z81515; PIDN:CAB04197.1; GSPDB:IGN00020; CESP:F2
C:Experimental source: clone F26H11
C:Genetics:
A:Gene: CESP:F26H11.2
A:Map position: 2
A:Insertions: 56/3; 154/2; 373/2; 417/3; 505/2; 596/1; 703/2; 847/3; 922/3; 1034/2; 1078/2;
Query Match 59.4%; Score 41; DB 2; Length 1711;
Best Local Similarity 69.2%; Pred. No. 42;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 DKSESTSGAGRRR 14
DB 82 DPSESTSSRRR 94

RESULT 14
T31422
C-terminal domain-binding protein RA9 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31422
R:Yuryev, A.; Patuturajan, M.; Litington, Y.; Joshi, R.V.; Gentile, C.; Gebbara, M.; Cordé
Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996
A:Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts with
A:Reference number: Z21024; MUID:96293459; PMID:8692929
A:Accession: T31422
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1473 <YUR>
A:Cross-references: UNIPROT:Q63625; EMBL:U49057; NID:G1438533; PID:G1438534; PIDN:AAC526;
A:Experimental source: hippocampus

Query Match 56.5%; Score 39; DB 2; Length 1473;
Best Local Similarity 57.1%; Pred. No. 85;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDKSESTSGAGRRR 14
DB 944 MDKSESTSGRRR 957

RESULT 15
B83765
hypochemical protein BH0922 (imported) - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: B83765
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hixan
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: B83765
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-38 <STO>
A:Cross-references: UNIPROT:Q9XED1; GB:AP001510; GB:BA000004; NID:G10173440; PIDN:BA046;
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0922

Query Match 55.1%; Score 38; DB 2; Length 38;
Best Local Similarity 53.8%; Pred. No. 3.5;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDKSESTSGAGRRR 13
DB 1 MDKQKQWABGRNR 13

Search completed: December 5, 2004, 08:05:50.
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2004, 07:59:17 ; Search time 91 Seconds

(without alignments)
88.519 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSGRNR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: UniProt 02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 2 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 3 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 4 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 5 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 6 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 7 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 8 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 9 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 10 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 11 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 12 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 13 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 14 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 15 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 16 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 17 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 18 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 19 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 20 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 21 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 22 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 23 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 24 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 25 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 26 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 27 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 28 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 29 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 30 | 69 | 100.0 | 217 | 2 | Q6T7D4 |
| 31 | 69 | 100.0 | 217 | 2 | Q6T7D4 |

| | | | | | |
|----|----|-------|-----|---|--------|
| 32 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 33 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 34 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 35 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 36 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 37 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 38 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 39 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 40 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 41 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 42 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 43 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 44 | 69 | 100.0 | 218 | 2 | Q76U37 |
| 45 | 69 | 100.0 | 218 | 2 | Q76U37 |

ALIGNMENTS

| | | | | |
|---|--|--------------|------|---------|
| RESULT 1 | Q6T7D4 | PRELIMINARY; | PRT; | 217 AA. |
| ID | Q6T7D4 | PRELIMINARY; | PRT; | 217 AA. |
| AC | Q6T7D4 | PRELIMINARY; | PRT; | 217 AA. |
| DT | 05-JUL-2004 (Tremblrel. 27, Created) | | | |
| DT | 05-JUL-2004 (Tremblrel. 27, Last sequence update) | | | |
| DT | 05-JUL-2004 (Tremblrel. 27, Last annotation update) | | | |
| DE | Coat protein. | | | |
| OS | Cucumber mosaic virus (cucumber mosaic cucumovirus). | | | |
| OC | Virusess; ssRNA positive-strand viruses, no DNA stage; Bromoviridae; | | | |
| OX | NCBI_TaxID=12305; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Yan L., Xu Z., Goldbach R., Chen K., Prins M.; | | | |
| RL | Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AY429437; AAR89478.1; " | | | |
| DR | GO; GO:0019028; C:Viral capsid; IEA. | | | |
| DR | GO; GO:0005198; F:Structural molecule activity; IEA. | | | |
| DR | InterPro; IPR000247; Cucumovirus_coat. | | | |
| DR | InterPro; IPR008975; Viral_cap_coat. | | | |
| DR | Pfam; PF00760; Cucumo_coat; 1. | | | |
| DR | PRINTS; PR00222; CUCUMOCOAT. | | | |
| DR | ProDom; PD001284; Cucumovirus_coat; 1. | | | |
| KW | Coat protein. | | | |
| SC | SEQUENCE 217 AA; 24015 MW; 32D0035B4F20E891 CRC64; | | | |
| Query Match | 100.0%; Score 69; DB 2; Length 217; | | | |
| Best Local Similarity | 100.0%; Pred. No. 0.00013; | | | |
| Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | |
| QY | 1 MDKSESTSGRNR 14 | | | |
| DB | 1 MDKSESTSGRNR 14 | | | |
| RESULT 2 | Q66133 | PRELIMINARY; | PRT; | 217 AA. |
| ID | Q66133 | PRELIMINARY; | PRT; | 217 AA. |
| AC | Q66133 | PRELIMINARY; | PRT; | 217 AA. |
| DT | 01-NOV-1996 (Tremblrel. 01, Created) | | | |
| DT | 01-NOV-1996 (Tremblrel. 01, Last sequence update) | | | |
| DT | 01-OCT-2003 (Tremblrel. 25, Last annotation update) | | | |
| DE | Coat protein. | | | |
| OS | Cucumber mosaic virus (cucumber mosaic cucumovirus). | | | |
| OC | Virusess; ssRNA positive-strand viruses, no DNA stage; Bromoviridae; | | | |
| OX | NCBI_TaxID=12305; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Reichel H., Marino L., Kummert J., Belalcazar S., Narvaez J.; | | | |
| RT | "Characterization del gen de la proteina de la capsida de dos | | | |
| RT | aislamentos del virus del mosaico del pepino (CMV), obtenidos de | | | |
| RT | platano y banana (Musa spp.)."; | | | |

```
RL Revista Corporea 1:1-5(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Marino-Ramirez L.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U32859; AAB50176.1; -.
DR PIR; JC6073; JC6073.
DR PIR; JC6075; JC6075.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 217 AA; 24015 MW; 7251B7E67192DCAB CRC64;

Query Match 100.0%; Score 69; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGAGNRR 14
DB 1 MDKSESTSGAGNRR 14

RESULT 3
OQ07A0 PRELIMINARY; PRT; 217 AA.
AC OQ07A0;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Coat protein.
OS Banana mosaic virus.
OC Viruses; unclassified viruses.
OX NCBI_TaxID=179820;
RN [1]
RP SEQUENCE FROM N.A.
RA Daolin D., Jie S., Peng Z., Zhixin L., Xiaodong D., Xueqing Z.;
RL "Cloning and Reconstruction of a Expression Vector for the Banana
RT Mosaiic Virus Coat Protein Gene.";
RL Guangxi Zhi Wu 0:0-0(2002).
DR EMBL; AF444252; AAL48223.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 217 AA; 23739 MW; 3873A80567D3B3AE CRC64;

Query Match 100.0%; Score 69; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGAGNRR 14
DB 1 MDKSESTSGAGNRR 14

RESULT 4
AAR89478 PRELIMINARY; PRT; 217 AA.
AC AAR89478;
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
DE Coat protein.
OS Cucumber mosaic virus (cucumber mosaic cucumovirus).
SQ
```

```
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=12305;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CS;
RA Yan L., Xu Z., Goldbach R., Chen K., Pines M.;
RT "Complete nucleotide sequence of cucumber mosaic virus (CS isolate)
RT RNA3 ";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY429437; AAR89478.1; -.
KW Coat protein.
SQ SEQUENCE 217 AA; 24015 MW; 32D0035B4F20E891 CRC64;

Query Match 100.0%; Score 69; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGAGNRR 14
DB 1 MDKSESTSGAGNRR 14

RESULT 5
COAT_CMVAS STANDARD; PRT; 218 AA.
AC 066154;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumber mosaic virus (strain As) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117118;
RN [1]
RP SEQUENCE FROM N.A.
RA Hyon S., Park Y.I.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.
CC -----
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CC -----
DR EMBL; X77855; CAA54846.1; -.
DR PIR; S42098; S42098.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24044 MW; E6BEC2E3D4CD73BF CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGAGNRR 14
DB 1 MDKSESTSGAGNRR 14

RESULT 6
COAT_CMVBA STANDARD; PRT; 218 AA.
AC 066135;
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DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumovirus mosaic virus (strain Banana) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
CC Cucumovirus.
XX NCBI_TaxID=117120;
RN [1]
RP SEQUENCE FROM N.A.
RA Gafny R., Wexler A., Mawaasi M., Israeli Y., Bar-Joseph M.;
RT "Natural infection of banana by a satellite-containing strain of
RT cucumber mosaic virus.";
RL Phytoparasitica 24:49-56 (1996).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.
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-----
DR EMBL; U43888; AAA87044.1; -
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KM Coat protein.
SQ SEQUENCE 218 AA; 24174 MW; 9BB4FEB212A21223 CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGAGNRR 14
DQ 1 MDKSESTSGAGNRR 14

RESULT 7
COAT_CWVC7 STANDARD; PRT; 218 AA.
AC 040983;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumovirus mosaic virus (strain C7-2) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
CC Cucumovirus.
XX NCBI_TaxID=117117;
RN [1]
RP SEQUENCE FROM N.A.
RA Chaumpiluk P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,
RA Suzuki K., Mise K., Inouye N., Okuno T., Furusawa I.;
RT "Six new subgroup I members of Japanese cucumber mosaic virus as
RT determined by nucleotide sequence analysis on RNAs' s cDNAs.";
RL Ann. Phytopathol. Soc. Jpn. 62:40-44 (1996).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.
-----
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DR EMBL; D42079; BAA07675.1; -
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KM Coat protein.
SQ SEQUENCE 218 AA; 24033 MW; 16D96022D1A26FD8 CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGAGNRR 14
DQ 1 MDKSESTSGAGNRR 14

RESULT 8
COAT_CWVC8 STANDARD; PRT; 218 AA.
AC 066143;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumovirus mosaic virus (strain CS) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
CC Cucumovirus.
XX NCBI_TaxID=117109;
RN [1]
RP SEQUENCE FROM N.A.
RA Chaumpiluk P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,
RA Suzuki K., Mise K., Inouye N., Okuno T., Furusawa I.;
RT "Six new subgroup I members of Japanese cucumber mosaic virus as
RT determined by nucleotide sequence analysis on RNAs' s cDNAs.";
RL Ann. Phytopathol. Soc. Jpn. 62:40-44 (1996).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.
-----
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-----
DR EMBL; D28489; BAA05851.1; -
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KM Coat protein.
SQ SEQUENCE 218 AA; 24157 MW; 76F6BDCE9628F683 CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGAGNRR 14
DQ 1 MDKSESTSGAGNRR 14

RESULT 9
COAT_CWVC9 STANDARD; PRT; 218 AA.
AC 000259;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

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OC Coat protein (Capsid protein) (CP).
OS Cucumbr mosaic virus (strain FC) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=31717;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92012983; PubMed=1919534;
RA Shintaku M.;
RT "Coat protein gene sequences of two cucumber mosaic virus strains
RT reveal a single amino acid change correlating with chlorosis
RT induction."
RL J. Gen. Virol. 72:2587-2589 (1991).
CC -----
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CC -----
CC EMBL; D10544; BAA01403.1; -.
DR PIR; J01253; J01253.
DR InterPro; IPR000247; Cucumovirus coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
DR KW
SQ SEQUENCE 218 AA; 24130 MW; C4B7CFB12F2A7CAB CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDSKSTSGAGNRR 14
Db 1 MDSKSTSGAGNRR 14
|||||
|

RESULT 10
COAT_CMVFT STANDARD; PRT; 218 AA.
ID COAT_CMVFT
AC Q66140;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbr mosaic virus (strain FT) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117112;
RN [1]
RP SEQUENCE FROM N.A.
RA Champulux P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,
RA Suzuki K., Wase K., Inouye N., Okuno T., Furusawa I.;
RT "Six new subgroup I members of Japanese cucumber mosaic virus as
RT determined by nucleotide sequence analysis on RNAs' s cDNAs.";
RT Ann. Phytopathol. Soc. Jpn. 62:40-44 (1996).
CC -----
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.
CC -----
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CC -----
CC EMBL; D28487; BAA05847.1; -.
DR InterPro; IPR000247; Cucumovirus_coat.

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DR InterPro: IPR008975; Viral_cap_coat.
DR Pfam: PF00760; Cucumo_coat; 1.
DR PRINTS: PR00222; CUCUMOCOAT.
DR ProDom: PD001284; Cucumovirus_coat; 1.
DR Coat protein.
SQ SEQUENCE 218 AA; 24160 MW; 5D3B98298EA3997 CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00033; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 MDKSESTSAGRNRR 14
   |||||
   |||||
   |||||
Db 1 MDKSESTSAGRNRR 14

RESULT 11
COAT_CNV11 STANDARD; PRT; 218 AA.
AC
PI4767;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbers mosaic virus (strain 117F) (CMV), and
OS Cucumbers mosaic virus (strain FNV) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=12308, 12307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=117F;
RX MEDLINE=90098885; PubMed=2602158;
RA Noel M.J.T., Ben Tahar S.;
RT "Nucleotide sequence of the coat protein gene and flanking regions of
RT cucumber mosaic virus (CMV) strain 117F.";
RL Nucleic Acids Res. 17:10492-10492(1989).
RN [2]
RP ERRATUM.
RX MEDLINE=90206832; PubMed=2320436;
RA Noel M.J.T., Ben Tahar S.;
RL Nucleic Acids Res. 18:1332-1332(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FNV;
RX MEDLINE=91037954; PubMed=2230731;
RA Owen J., Shintaku M., Aeschleman P., Tahar S., Palukaitis P.;
RT "Nucleotide sequence and evolutionary relationships of cucumber mosaic
RT virus (CMV) strains; CMV RNA 3.";
RL J. Gen. Virol. 71:2243-2249(1990).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.
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CC -----
DR EMBL: X16386; CAA34422.1; -.
DR EMBL: D10538; BAA01397.1; -.
DR PIR: S09663; S09663.
DR InterPro: IPR000247; Cucumovirus_coat.
DR InterPro: IPR008975; Viral_cap_coat.
DR Pfam: PF00760; Cucumo_coat; 1.
DR PRINTS: PR00222; CUCUMOCOAT.
DR ProDom: PD001284; Cucumovirus_coat; 1.
DR Coat protein.
SQ SEQUENCE 218 AA; 24140 MW; C4B4FCB21F197F98 CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;

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QY 1 MDKSESTSGRNR 14
|||||

Db 1 MDKSESTSGRRR 14

RESULT 15

COAT_CMVN STANDARD; PRT; 218 AA.

ID COAT_CMVN

AC 066138;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Coat protein (Capsid protein) (CP).

OS Cucumbers; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;

OC Cucumovirus.

OC NCBI_Taxid=117123;

OX NCBI_Taxid=117123;

RN [1]

RA SEQUENCE FROM N.A. Chaumplik P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,

RA Suzuki K., Mise K., Inouye N., Okuno T., Furusawa I.;

RT "Six new subgroup I members of Japanese cucumber mosaic virus as

determined by nucleotide sequence analysis on RNA3's cDNAs.";

RL Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).

CC -I- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein

CC family.

CC

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CC EMBL: D26486; BAA05845.1; -

DR InterPro; IPR000247; Cucumovirus_coat.

DR InterPro; IPR008975; Viral_cap_coat.

DR Pfam; PF00760; Cucumo_coat; 1.

DR PRINTS; PR00222; CUCUMOCOAT.

DR ProDom; PD001284; Cucumovirus_coat; 1.

KM Coat protein.

SQ SEQUENCE 218 AA; 24078 MW; 0BA67C84D8F41B22 CRC64;

Query Match 100.0%; Score 69; DB 1; Length 218;

Best local similarity 100.0%; Pred. No. 0.00013;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRRR 14

Db 1 MDKSESTSGRRR 14

Search completed: December 5, 2004, 08:07:27
Job time : 92 secs

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OM protein - protein search, using sw model

Run on: December 5, 2004, 08:00:12 ; Search time 23 Seconds
(without alignments)
40.367 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSGRNR 14

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patente AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PTUTS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--|
| 1 | 69 | 100.0 | 217 | 6 | 5422259-2 Patent No. 5422259 |
| 2 | 69 | 100.0 | 218 | 1 | US-08-398-209-2 Sequence 2, Appli |
| 3 | 69 | 100.0 | 218 | 1 | US-08-398-209-4 Sequence 4, Appli |
| 4 | 69 | 100.0 | 218 | 2 | US-08-553-619B-3 Sequence 3, Appli |
| 5 | 69 | 100.0 | 218 | 3 | US-08-875-233-2 Sequence 2, Appli |
| 6 | 69 | 100.0 | 218 | 3 | US-08-875-233-4 Sequence 4, Appli |
| 7 | 69 | 100.0 | 218 | 3 | US-08-875-233-6 Sequence 6, Appli |
| 8 | 69 | 100.0 | 218 | 3 | US-08-875-233-15 Sequence 15, Appli |
| 9 | 69 | 100.0 | 218 | 3 | US-09-127-742-2 Sequence 2, Appli |
| 10 | 69 | 100.0 | 218 | 3 | US-09-127-742-4 Sequence 4, Appli |
| 11 | 69 | 100.0 | 218 | 6 | 5422259-4 Patent No. 5422259 |
| 12 | 64 | 92.8 | 218 | 3 | US-08-875-233-10 Sequence 10, Appli |
| 13 | 64 | 92.8 | 218 | 4 | US-09-513-999C-4827 Sequence 4827, Ap |
| 14 | 63 | 56.5 | 66 | 3 | US-08-961-564A-5 Sequence 5, Appli |
| 15 | 63 | 56.5 | 172 | 3 | US-09-383-080-3 Sequence 3, Appli |
| 16 | 38 | 55.1 | 172 | 3 | US-08-858-937-3 Sequence 3, Appli |
| 17 | 37 | 53.6 | 303 | 4 | US-09-328-352-8049 Sequence 8049, Ap |
| 18 | 37 | 53.6 | 471 | 4 | US-09-328-352-7581 Sequence 7581, Ap |
| 19 | 36 | 52.2 | 81 | 4 | US-09-489-039A-9928 Sequence 9928, Ap |
| 20 | 36 | 52.2 | 232 | 3 | US-08-869-674-2 Sequence 2, Appli |
| 21 | 36 | 52.2 | 232 | 3 | US-09-213-010-2 Sequence 2, Appli |
| 22 | 36 | 52.2 | 232 | 4 | US-09-213-011-2 Sequence 2, Appli |
| 23 | 36 | 52.2 | 232 | 4 | US-09-583-110-4554 Sequence 4554, Ap |
| 24 | 36 | 52.2 | 282 | 4 | US-09-248-796A-28057 Sequence 28057, A |
| 25 | 36 | 52.2 | 802 | 4 | US-09-889-746-4 Sequence 4, Appli |
| 26 | 36 | 52.2 | 3080 | 6 | 5223423-4 Patent No. 5223423 |
| 27 | 35.5 | 51.4 | 852 | 4 | US-09-585-858-19 Sequence 19, Appli |

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| 28 | 35.5 | 51.4 | 1194 | 2 | US-08-680-326-35 Sequence 35, Appli |
| 29 | 35 | 50.7 | 91 | 4 | US-09-543-681A-6613 Sequence 6613, Ap |
| 30 | 35 | 50.7 | 163 | 4 | US-09-252-991A-29098 Sequence 29098, A |
| 31 | 35 | 50.7 | 213 | 4 | US-09-252-991A-30768 Sequence 30768, A |
| 32 | 35 | 50.7 | 218 | 3 | US-08-875-233-13 Sequence 12, Appli |
| 33 | 35 | 50.7 | 218 | 3 | US-08-875-233-13 Sequence 12, Appli |
| 34 | 35 | 50.7 | 248 | 4 | US-09-270-767-40111 Sequence 40111, A |
| 35 | 35 | 50.7 | 248 | 4 | US-09-270-767-55327 Sequence 55327, A |
| 36 | 35 | 50.7 | 266 | 4 | US-09-252-991A-32512 Sequence 32512, A |
| 37 | 35 | 50.7 | 266 | 4 | US-09-252-991A-32512 Sequence 32512, A |
| 38 | 35 | 50.7 | 266 | 4 | US-09-252-991A-32512 Sequence 32512, A |
| 39 | 35 | 50.7 | 499 | 3 | US-09-457-040B-13 Sequence 13, Appli |
| 40 | 35 | 50.7 | 499 | 3 | US-09-457-040B-13 Sequence 13, Appli |
| 41 | 35 | 50.7 | 561 | 4 | US-09-905-999-21 Sequence 21, Appli |
| 42 | 35 | 50.7 | 571 | 4 | US-09-812-079A-2 Sequence 2, Appli |
| 43 | 35 | 50.7 | 579 | 4 | US-09-914-259-32 Sequence 32, Appli |
| 44 | 35 | 50.7 | 579 | 4 | US-09-171-699-6 Sequence 6, Appli |
| 45 | 35 | 50.7 | 752 | 4 | US-09-171-699-8 Sequence 8, Appli |
| | | | | | US-08-605-541B-12 Sequence 12, Appli |
| | | | | | US-09-919-039-235 Sequence 235, App |

ALIGNMENTS

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RESULT 1
5422259-2
: Patent No. 5422259
: APPLICANT: DE BOTH, MICHEL, BEN TAHAR, SOPHIA, NOEL, MARIANNE;
: PERRET, JOEL
: TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE
: SPECIES CUCUMIS MELO
: NUMBER OF SEQUENCES: 4
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/27,563
: FILING DATE: 05-MAR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 566,255
: FILING DATE: 13-AUG-1990
: SEQ ID NO:2
: LENGTH: 217
5422259-2

Query Match      100.0%; Score 69; DB 6; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 MDKSESTSGRNR 14
Db      1 MDKSESTSGRNR 14

RESULT 2
US-08-398-209-2
: Sequence 2, Application US/08398209
: Patent No. 5789656
: GENERAL INFORMATION:
: APPLICANT: Deboth, Michel
: APPLICANT: No. 57896561, Marianne
: APPLICANT: Ben Tahar, Sophia
: TITLE OF INVENTION: Transgenic Plants Belonging to the
: SPECIES CUCUMIS MELO
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merchant & Gould
: STREET: 90 South 7th Street, 3100 NO. 5789656west Center
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,209
FILING DATE: 05-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,563
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/566,255
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 8910848
FILING DATE: 11-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A.
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.21US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-398-209-2

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14
DB 1 MDKSESTAGRNRR 14

RESULT 3
US-08-398-209-4
Sequence 4, Application US/08398209
Patent No. 5789656
GENERAL INFORMATION:
APPLICANT: Deboth, Michel
APPLICANT: No. 57896561, Marianne
APPLICANT: Ben Tahar, Sophia
APPLICANT: Perret, Joel
TITLE OF INVENTION: Transgenic Plants Belonging to the
TITLE OF INVENTION: Species Cucumis Melo
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5789656west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,209
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,563
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/566,255
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 8910848
FILING DATE: 11-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A.
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.21US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-398-209-4

Query Match 100.0%; Score 69; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDKSESTAGRNRR 14

RESULT 4
US-08-553-619B-3
Sequence 3, Application US/08553619B
Patent No. 5919705
GENERAL INFORMATION:
APPLICANT: Dehaan, Petrus T.
TITLE OF INVENTION: Virus Resistant Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: No. 5919705artis Crop Protection
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,619B
FILING DATE: December 1, 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 137-1082/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/354-3588
TELEFAX: 415/857-1125
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-619B-3

Query Match 100.0%; Score 69; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTAGRNRR 14
DB 1 MDKSESTAGRNRR 14

RESULT 5
US-08-875-233-2
Sequence 2, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSES: Rokey, Milanow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-2

Query Match 100.0%; Score 69; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 6
US-08-875-233-4
Sequence 4, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSES: Rokey, Milanow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-4

Query Match 100.0%; Score 69; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 7
US-08-875-233-6
Sequence 6, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSES: Rokey, Milanow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-6

Query Match 100.0%; Score 69; DB 3; Length 218;

Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
Db 1 MDKSESTSGRNR 14

RESULT 8

US-08-875-233-15
Sequence 15, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60689
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-15

Query Match 100.0%; Score 69; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
Db 1 MDKSESTSGRNR 14

RESULT 9

US-09-127-742-2
Sequence 2, Application US/09127742A
Patent No. 6198022
GENERAL INFORMATION:
APPLICANT: DE BOTH, MICHAEL
APPLICANT: NOEL, MARIANNE
APPLICANT: TAHAR, SOPHIA BEN
APPLICANT: PERRET, JOEL
APPLICANT: BIOSEM
TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE SPECIES CUCUMIS MELO
FILE REFERENCE: 8076.21USD2
CURRENT APPLICATION NUMBER: US/09/127,742A
CURRENT FILING DATE: 1998-08-03

EARLIER APPLICATION NUMBER: 08/398,209
EARLIER FILING DATE: 1995-03-02
EARLIER APPLICATION NUMBER: 08/027,563
EARLIER FILING DATE: 1993-03-05
EARLIER APPLICATION NUMBER: 07/566,255
EARLIER FILING DATE: 1990-08-13
EARLIER APPLICATION NUMBER: FR 89 10848
EARLIER FILING DATE: 1989-08-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 218
TYPE: PRT
ORGANISM: cucumber mosaic virus
US-09-127-742-2

Query Match 100.0%; Score 69; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
Db 1 MDKSESTSGRNR 14

RESULT 10

US-09-127-742-4
Sequence 4, Application US/09127742A
Patent No. 6198022
GENERAL INFORMATION:
APPLICANT: DE BOTH, MICHAEL
APPLICANT: NOEL, MARIANNE
APPLICANT: TAHAR, SOPHIA BEN
APPLICANT: PERRET, JOEL
APPLICANT: BIOSEM
TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE SPECIES CUCUMIS MELO
FILE REFERENCE: 8076.21USD2
CURRENT APPLICATION NUMBER: US/09/127,742A
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: 08/398,209
EARLIER FILING DATE: 1995-03-02
EARLIER APPLICATION NUMBER: 08/027,563
EARLIER FILING DATE: 1993-03-05
EARLIER APPLICATION NUMBER: 07/566,255
EARLIER FILING DATE: 1990-08-13
EARLIER APPLICATION NUMBER: FR 89 10848
EARLIER FILING DATE: 1989-08-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 218
TYPE: PRT
ORGANISM: cucumber mosaic virus
US-09-127-742-4

Query Match 100.0%; Score 69; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
Db 1 MDKSESTSGRNR 14

RESULT 11

5422259-4
Patent No. 5422259
APPLICANT: DE BOTH, MICHAEL, BEN TAHAR, SOPHIA, NOEL, MARIANNE;
APPLICANT: PERRET, JOEL
TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE
SPECIES CUCUMIS MELO
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/27,563
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 566,255
FILING DATE: 13-AUG-1990
SEQ ID NO: 4
LENGTH: 218
5422259-4

Query Match 100.0%; Score 69; DB 6; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14

RESULT 12

US-08-875-233-10
Sequence 10, Application US/08875233
Patent No. 6127601

GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John P
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milanow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Steetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60689
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-10

Query Match 92.8%; Score 64; DB 3; Length 218;
Best Local Similarity 92.9%; Pred. No. 0.0009;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14

RESULT 13
US-09-513-999C-4827
Sequence 4827, Application US/09513999C
Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclet, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent .pm
SEQ ID NO 4827
LENGTH: 64
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-4827

Query Match 56.5%; Score 39; DB 4; Length 64;
Best Local Similarity 58.3%; Pred. No. 6.6;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 KSESTSGRNR 14
DB 53 QSESTNGKMR 64

RESULT 14
US-08-961-564A-5
Sequence 5, Application US/08961564A
Patent No. 614515

GENERAL INFORMATION:
APPLICANT: WU, SHUIJIAN
APPLICANT: SWEET, RAYMOND
TITLE OF INVENTION: TRUNEH, ALEMGED
TITLE OF INVENTION: PIGRL-1, A MEMBER OF IMMUNOGLOBULIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,564A
FILING DATE: 30-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/056,935
FILING DATE: 25-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70236
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-961-564A-5

Query Match 56.5%; Score 39; DB 3; Length 66;
Best Local Similarity 72.7%; Pred. No. 6.8;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DKSESTAGRN 12
|||:||||
Db 27 DKETKSAGRN 37

RESULT 15

US-09-382-080-3
; Sequence 3, Application US/09382080
; Patent No. 6087333
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: DISEASE ASSOCIATED ACIDIC PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09382,080
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,937
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0308 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1276649
; US-09-382-080-3

Query Match 55.1%; Score 38; DB 3; Length 172;
Best Local Similarity 70.0%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 ESTSAGRRR 14
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Db 87 DSTWGRNR 96

Search completed: December 5, 2004, 08:07:56
Job time : 24 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: December 5, 2004, 08:04:17 ; Search time 353 Seconds
(without alignments)
14.144 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTASGRNR 14

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 35623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppa/US09C_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | ID | Description |
|------------|-------|--------------|-----------------------------|--------------------|
| 1 | 69 | 100.0 | 218 13 US-10-011-033-2 | Sequence 2, Appl1 |
| 2 | 69 | 100.0 | 218 13 US-10-011-033-4 | Sequence 4, Appl1 |
| 3 | 69 | 100.0 | 218 13 US-10-011-033-6 | Sequence 6, Appl1 |
| 4 | 69 | 100.0 | 218 13 US-10-011-033-15 | Sequence 15, Appl1 |
| 5 | 64 | 92.8 | 218 13 US-10-011-033-10 | Sequence 10, Appl1 |
| 6 | 43 | 62.3 | 225 16 US-10-437-963-189118 | Sequence 189118, |
| 7 | 41 | 59.4 | 193 16 US-10-437-963-135827 | Sequence 135827, |
| 8 | 41 | 59.4 | 254 16 US-10-437-963-150193 | Sequence 150193, |
| 9 | 41 | 59.4 | 273 16 US-10-437-963-190100 | Sequence 190100, |
| 10 | 40 | 58.0 | 159 15 US-10-424-599-184959 | Sequence 184959, |
| 11 | 40 | 58.0 | 202 17 US-10-425-115-190976 | Sequence 190976, |
| 12 | 39 | 56.5 | 68 14 US-10-029-386-31499 | Sequence 31499, A |
| 13 | 39 | 56.5 | 103 17 US-10-425-115-188688 | Sequence 188688, |

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| 14 | 39 | 56.5 | 1104 14 US-10-369-493-4135 | Sequence 4135, Ap |
| 15 | 38 | 55.1 | 109 17 US-10-425-115-253470 | Sequence 253470, |
| 16 | 38 | 55.1 | 121 17 US-10-425-115-249986 | Sequence 249986, |
| 17 | 38 | 55.1 | 197 15 US-10-452-858C-31 | Sequence 31, Appl |
| 18 | 38 | 55.1 | 251 16 US-10-437-963-109979 | Sequence 109979, |
| 19 | 38 | 55.1 | 319 14 US-10-156-761-11072 | Sequence 11072, A |
| 20 | 38 | 55.1 | 371 15 US-10-425-114-50396 | Sequence 50396, A |
| 21 | 38 | 55.1 | 408 17 US-10-425-115-357819 | Sequence 357819, |
| 22 | 38 | 55.1 | 493 15 US-10-425-114-63801 | Sequence 63801, A |
| 23 | 38 | 55.1 | 493 17 US-10-425-115-201525 | Sequence 201525, |
| 24 | 38 | 55.1 | 530 16 US-10-437-963-193875 | Sequence 193875, |
| 25 | 38 | 55.1 | 703 15 US-10-424-599-247762 | Sequence 247762, |
| 26 | 38 | 55.1 | 1511 14 US-10-369-493-22496 | Sequence 22496, A |
| 27 | 38 | 55.1 | 19662 15 US-10-084-846A-6 | Sequence 151781, |
| 28 | 37 | 53.6 | 89 16 US-10-437-963-151781 | Sequence 151781, |
| 29 | 37 | 53.6 | 113 14 US-10-266-886-7 | Sequence 7, Appl1 |
| 30 | 37 | 53.6 | 142 16 US-10-437-963-110739 | Sequence 110739, |
| 31 | 37 | 53.6 | 147 16 US-10-767-701-56363 | Sequence 56363, A |
| 32 | 37 | 53.6 | 183 15 US-10-425-114-51049 | Sequence 51049, A |
| 33 | 37 | 53.6 | 198 16 US-10-437-963-129622 | Sequence 129622, |
| 34 | 37 | 53.6 | 202 16 US-10-437-963-110737 | Sequence 110737, |
| 35 | 37 | 53.6 | 205 15 US-10-424-599-215773 | Sequence 215773, |
| 36 | 37 | 53.6 | 223 9 US-09-925-300-1246 | Sequence 1246, Ap |
| 37 | 37 | 53.6 | 265 10 US-09-925-302-559 | Sequence 559, App |
| 38 | 37 | 53.6 | 265 10 US-09-925-302-559 | Sequence 559, App |
| 39 | 37 | 53.6 | 275 15 US-10-282-122A-49014 | Sequence 49014, A |
| 40 | 37 | 53.6 | 276 15 US-10-374-780A-1883 | Sequence 1883, Ap |
| 41 | 37 | 53.6 | 277 14 US-10-369-493-4258 | Sequence 4258, Ap |
| 42 | 37 | 53.6 | 281 16 US-10-437-963-136159 | Sequence 136159, |
| 43 | 37 | 53.6 | 375 17 US-10-425-115-323368 | Sequence 323368, |
| 44 | 37 | 53.6 | 448 16 US-10-437-963-169865 | Sequence 169865, |
| 45 | 37 | 53.6 | 672 14 US-10-291-265-455 | Sequence 455, App |

ALIGNMENTS

RESULT 1
US-10-011-033-2
; Sequence 2, Application US/10011033
; Publication No. US20020124286A1
; GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L.
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSER: Rockey, Milanow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stebson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011.033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875.233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-011-033-2

Query Match 100.0%; Score 69; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14

RESULT 2

US-10-011-033-4
Sequence 4, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESS: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Steetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-011-033-4

Query Match 100.0%; Score 69; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14

RESULT 3

US-10-011-033-6
Sequence 6, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESS: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Steetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-011-033-6

Query Match 100.0%; Score 69; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14

RESULT 4

US-10-011-033-15
Sequence 15, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESS: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Steetson, Suite 4700
CITY: Chicago

STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-011-033-15
Query Match 100.0%; Score 69; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKSESTSGAGNRR 14
1 MDKSESTSGAGNRR 14
Db 1 MDKSESTSGAGNRR 14
RESULT 5
US-10-011-033-10
Sequence 10, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-011-033-10
Query Match 92.8%; Score 64; DB 13; Length 218;
Best Local Similarity 92.9%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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1 MDKSESTSGAGNRR 14
Db 1 MDKSESTSGAGNRR 14
RESULT 6
US-10-437-963-189118
Sequence 189118, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yinhua
APPLICANT: Cao, Yongwei
Wu, Wei
APPLICANT: Boukharov, Andrey A.
Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
File Reference: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 189118
LENGTH: 225
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_85657C.1.pep
US-10-437-963-189118
Query Match 62.3%; Score 43; DB 16; Length 225;
Best Local Similarity 57.1%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 MDKSESTSGAGNRR 14
1 MDKSESTSGAGNRR 14
Db 19 MSNSDKTTAGRHRR 32
RESULT 7
US-10-437-963-135827
Sequence 135827, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yinhua
APPLICANT: Cao, Yongwei
Wu, Wei
APPLICANT: Boukharov, Andrey A.
Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
File Reference: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 135827
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Oryza sativa

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_37465C.1.pep

US-10-437-963-135827

Query Match 59.4%; Score 41; DB 16; Length 193;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSESTSGNR 12
DB 1 MDSESTSGKD 12

RESULT 8

US-10-437-963-150193
; Sequence 150193, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 150193
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_50452C.1.pep

US-10-437-963-150193

Query Match 59.4%; Score 41; DB 16; Length 254;
Best Local Similarity 50.0%; Pred. No. 67;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDSESTSGNR 14
DB 140 LKSKSTRNGKNKR 153

RESULT 9

US-10-437-963-190100
; Sequence 190100, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 190100
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Oryza sativa

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_86546C.1.pep

US-10-437-963-190100

Query Match 59.4%; Score 41; DB 16; Length 273;
Best Local Similarity 69.2%; Pred. No. 72;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 DKSESTSGNR 14
DB 203 DMSRSSNGNR 215

RESULT 10

US-10-424-599-184959
; Sequence 184959, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 184959
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_138032C.1.pep

US-10-424-599-184959

Query Match 58.0%; Score 40; DB 15; Length 159;
Best Local Similarity 88.9%; Pred. No. 62;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 STSGNR 14
DB 2 STSGQNR 10

RESULT 11

US-10-425-115-190976
; Sequence 190976, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 190976
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_105749C.1.pep

US-10-425-115-190976

Query Match 58.0%; Score 40; DB 17; Length 202;
Best Local Similarity 53.8%; Pred. No. 79;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 DKSESTSGRNR 14
DB 31 DRSEASAPGRGR 43

RESULT 12

US-10-029-386-31499
; Sequence 31499, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEGMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31499
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC020728.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
; OTHER INFORMATION: SWISSPROT HIT: P42285, EVALUATE 2.00e-20
US-10-029-386-31499

Query Match 56.5%; Score 39; DB 14; Length 68;
Best Local Similarity 58.3%; Pred. No. 39;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 KSESTSGRNR 14
DB 31 QSESTNGRNR 42

RESULT 13

US-10-425-115-188688
; Sequence 188688, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 188688
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_103673C.1.pep
US-10-425-115-188688

Query Match 56.5%; Score 39; DB 17; Length 103;
Best Local Similarity 50.0%; Pred. No. 59;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 MDKSESTSGRNR 14
DB 85 LDQSKTMSGRNR 98

RESULT 14

US-10-369-493-4135
; Sequence 4135, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianning
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4135
; LENGTH: 1104
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-4135

Query Match 56.5%; Score 39; DB 14; Length 1104;
Best Local Similarity 53.8%; Pred. No. 6.6e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 DKSESTSGRNR 14
DB 985 DKTEKRAAGRNTK 997

RESULT 15

US-10-425-115-253470
; Sequence 253470, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 253470
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_162747C.1.pep
US-10-425-115-253470

Query Match 55.1%; Score 38; DB 17; Length 109;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 KSESTSGRNR 14
DB 90 KKKTTTAGKNRK 101

Search completed: December 5, 2004, 08:13:54

Mon Dec 6 16:58:53 2004

us-09-857-841-4.rapb

Page 6

Job time : 353 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 06:06:43 ; Search time 1421 Seconds
(without alignments)
1763.796 Million cell updates/sec

Title: US-09-857-841-3
Perfect score: 53
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_to:*
11: gb_sts:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 53 | 100.0 | 53 | BD261798 | BD261798 Enhanceme |
| 2 | 46 | 86.8 | 771 | AR111976 | AR111976 Sequence |
| 3 | 46 | 86.8 | 772 | AR111981 | AR111981 Sequence |
| 4 | 46 | 86.8 | 792 | AR111975 | AR111975 Sequence |
| 5 | 45.8 | 86.4 | 130 | AR031575 | AR031575 Sequence |
| 6 | 45.8 | 86.4 | 130 | AR065687 | AR065687 Sequence |
| 7 | 45.8 | 86.4 | 130 | AR097446 | AR097446 Sequence |
| 8 | 45.8 | 86.4 | 130 | I49964 | I49964 Sequence 14 |
| 9 | 45.8 | 86.4 | 131 | AR031572 | AR031572 Sequence |
| 10 | 45.8 | 86.4 | 131 | AR065684 | AR065684 Sequence |
| 11 | 45.8 | 86.4 | 131 | AR097443 | AR097443 Sequence |
| 12 | 45.8 | 86.4 | 131 | I49961 | I49961 Sequence 11 |
| 13 | 45.8 | 86.4 | 152 | AR031570 | AR031570 Sequence |
| 14 | 45.8 | 86.4 | 152 | AR065682 | AR065682 Sequence |
| 15 | 45.8 | 86.4 | 152 | AR097441 | AR097441 Sequence |
| 16 | 45.8 | 86.4 | 152 | I49959 | I49959 Sequence 9 |
| 17 | 45.8 | 86.4 | 154 | AR031574 | AR031574 Sequence |
| 18 | 45.8 | 86.4 | 154 | AR065686 | AR065686 Sequence |
| 19 | 45.8 | 86.4 | 154 | AR097445 | AR097445 Sequence |

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| 20 | 45.8 | 86.4 | 154 | 6 | I49963 | I49963 Sequence 13 |
| 21 | 45.8 | 86.4 | 862 | 14 | CMU32859 | U32859 Cucurbit mo |
| 22 | 45.8 | 86.4 | 864 | 14 | CMU32858 | U32858 Cucurbit mo |
| 23 | 45.8 | 86.4 | 894 | 14 | MCVCPB | I36525 Cucurbit mo |
| 24 | 45.8 | 86.4 | 976 | 6 | A32131 | A32131 CMV capsid |
| 25 | 45.8 | 86.4 | 976 | 6 | AR021486 | AR021486 Sequence |
| 26 | 45.8 | 86.4 | 976 | 6 | AR138342 | AR138342 Sequence |
| 27 | 45.8 | 86.4 | 976 | 6 | AR364710 | AR364710 Sequence |
| 28 | 45.8 | 86.4 | 976 | 6 | BD000278 | BD000278 Transgeni |
| 29 | 45.8 | 86.4 | 1007 | 6 | A32133 | A32133 CMV capsid |
| 30 | 45.8 | 86.4 | 1007 | 6 | A39812 | A39812 Sequence 6 |
| 31 | 45.8 | 86.4 | 1007 | 6 | AR021487 | AR021487 Sequence |
| 32 | 45.8 | 86.4 | 1007 | 6 | AR138343 | AR138343 Sequence |
| 33 | 45.8 | 86.4 | 1007 | 6 | AR364711 | AR364711 Sequence |
| 34 | 45.8 | 86.4 | 1007 | 6 | AR430190 | AR430190 Sequence |
| 35 | 45.8 | 86.4 | 1007 | 6 | BD000279 | BD000279 Transgeni |
| 36 | 45.8 | 86.4 | 1007 | 14 | CMVCRN4 | X16366 Cucurbit mo |
| 37 | 45.8 | 86.4 | 1043 | 14 | CMU22821 | U22821 Cucurbit mo |
| 38 | 45.8 | 86.4 | 1043 | 14 | CMVCOATP | X77855 Cucurbit mo |
| 39 | 45.8 | 86.4 | 1066 | 6 | A67212 | A67212 Sequence 1 |
| 40 | 45.8 | 86.4 | 1067 | 6 | AR076864 | AR076864 Sequence |
| 41 | 45.8 | 86.4 | 1113 | 14 | CMO131624 | AJ131624 Cucurbit |
| 42 | 45.8 | 86.4 | 1115 | 14 | CMO131623 | AJ131623 Cucurbit |
| 43 | 45.8 | 86.4 | 1362 | 14 | MCVCPA | M22710 Cucurbit mo |
| 44 | 45.8 | 86.4 | 1379 | 6 | E01821 | E01821 cDNA encodi |
| 45 | 45.8 | 86.4 | 1696 | 6 | A41823 | A41823 Sequence 4 |

ALIGNMENTS

RESULT 1
LOCUS BD261798 53 bp DNA linear PAT 17-JUL-2003
DEFINITION Enhancement in protein production by higher plants using ubiquitin
or cucumber mosaic virus coating protein peptide.
ACCESSION BD261798.1 GI:33071566
VERSION BD261798
KEYWORDS UP 2002532098-A/2.
SOURCE Cucurbit mosaic virus (cucumber mosaic cucumovirus)
ORGANISM Cucurbit mosaic virus
Virusess; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
Cucumovirus.

REFERENCE 1 (bases 1 to 53)
Fang,R.X., Wu,J.L. and Chen,X.Y.
AUTHORS Enhancement in protein production by higher plants using ubiquitin
or cucumber mosaic virus coating protein peptide
TITLE Patent: JP 2002532098-A 2 02-OCT-2002;
JOURNAL INSTITUTE OF MOLECULAR AGRICULTURE

COMMENT

OS Cucurbit mosaic virus
PN UP 2002532098-A/2
PD 02-OCT-2002
PF 11-DEC-1998 JP 2000588378
PI RONG XIANG FANG, JUNG LIN WU, XIAO YING CHEN
PC C12N15/09,A01H5/00,C07K14/415,C07K19/00,C12N5/10,C12N15/00, PC
C12N5/00
CC Enhancement in protein production by higher plants using CC
ubiquitin or
CC cucumber mosaic virus coating protein peptide FH Key
Location/Qualifiers (6) . (47) .
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/mol_type="genomic DNA"
/db_xref="taxon:12305"

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Best Local Similarity 100.0%; Pred. No. 3.ee-11;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GATCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACGACT 53
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AR111976
LOCUS AR111976 771 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6127601.
ACCESSION AR111976
VERSION AR111976.1 GI:12828824
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 771)
AUTHORS Boeshore,M.L., McMaster,R.J., Triccoli,D.M., Reynolds,J.F. and Carney,K.J.
TITLE Plants resistant to C strains of cucumber mosaic virus
JOURNAL Patent: US 6127601-A 5 03-OCT-2000;
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.1e-08;
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Db 1 CCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 46
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RESULT 3
AR111981
LOCUS AR111981 772 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 14 from patent US 6127601.
ACCESSION AR111981
VERSION AR111981.1 GI:12828829
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 772)
AUTHORS Boeshore,M.L., McMaster,R.J., Triccoli,D.M., Reynolds,J.F. and Carney,K.J.
TITLE Plants resistant to C strains of cucumber mosaic virus
JOURNAL Patent: US 6127601-A 14 03-OCT-2000;
FEATURES
Location/Qualifiers
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OY 4 CCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 49
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Db 1 CCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 46
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RESULT 4
AR111975
LOCUS AR111975 792 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6127601.
ACCESSION AR111975
VERSION AR111975.1 GI:12828823
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 792)
AUTHORS Boeshore,M.L., McMaster,R.J., Triccoli,D.M., Reynolds,J.F. and Carney,K.J.
TITLE Plants resistant to C strains of cucumber mosaic virus
JOURNAL Patent: US 6127601-A 3 03-OCT-2000;
FEATURES
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/organism="unknown"
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OY 4 CCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 49
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Db 1 CCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 46
|||||
RESULT 5
AR031575
LOCUS AR031575 130 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 586384.
ACCESSION AR031575
VERSION AR031575.1 GI:5945864
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 586384-A 14 02-FEB-1999;
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Best Local Similarity 95.9%; Pred. No. 4.6e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 48 GATCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 96
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RESULT 6
AR065687
LOCUS AR065687 130 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5849548.
ACCESSION AR065687
VERSION AR065687.1 GI:5995903
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 14 15-DEC-1998;
FEATURES
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 86.4%; Score 45.8; DB 6; Length 130;
Best Local Similarity 95.9%; Pred. No. 4.6e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GATCCATGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 43
48 GAGTCATGACAAATCTGAATCAACCAAGTGTGTCGTAACCGTCGACG 96

| | | |
|------------|-------------------------------------|-----------------|
| RESULT 7 | | |
| AR097446 | | |
| LOCUS | AR097446 | 130 bp |
| DEFINITION | Sequence 14 from patent US 6071750. | DNA |
| | | linear |
| | | PAT 14-FEB-2001 |

| | |
|-----------|---|
| ORGANISM | Unknown. |
| REFERENCE | Unclassified. |
| AUTHORS | 1 (bases 1 to 130) |
| TITLE | Haseförf, J.; Brand, A.; Perriemon, N. and Goodman, H.M |
| JOURNAL | Cell ablation using trans-splicing ribozymes |
| FEATURES | Patent: US 6071730-A 14 06-JUN-2000; |
| source | Location/Qualifiers |
| | 1..130 |

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|--------------------------|--------------------------------------|
| ORIGIN | |
| Query Match | 86.4%; Score 45.8; DB 6; Length 130; |
| Best Local Similarity | 95.9%; Pred. No. 4,6e-08; |
| Matches 47; Conservative | 0; Mismatches 2; Indels 0; Gaps 0; |

| | | | |
|------------|-------------------------------------|------------|--------|
| RESULT 8 | | | |
| I49964 | I49964 | 130 bp | DNA |
| LOCUS | I49964 | | linear |
| DEFINITION | Sequence 14 from patent US 5641673. | | |
| ACCESSION | I49964 | | |
| VERSION | I49964.1 | GI:2472184 | |

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ORIGIN

Query Match      86.4%;   Score 45.8;   DB 6;   Length 130;
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Matches 47; Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0

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| | | | | |
|-----------------------|------------------------------------|--|-----|-----------------|
| Query Match | 86.4% | Score 45.8 | DB | Length 130 |
| Best Local Similarity | 95.9% | Pred. No. 4.6e-08 | | |
| Matches | 47 | Conservative | 0 | Mismatches 2 |
| | | | | Indels 0 |
| | | | | Gaps 0 |
| Qy | 1 | GATCCATGACAAATCTGAATCAACCAAGTGTGTCGTATCCCGTCGACG | 49 | |
| | | | | |
| | | | | |
| Db | 48 | GAGTCATGACAAATCTGAATCAACCAAGTGTGTCGTATCCCGTCGACG | 96 | |
| | | | | |
| | | | | |
| RESULT 9 | | | | |
| AR031572 | | | | |
| LOCUS | AR031572 | 131 bp | DNA | linear |
| DEFINITION | Sequence 11 from patent US 586384. | | | |
| | | | | PAT 29-SEP-1995 |

| | | | | | |
|------------|-------------------------------------|------------|-----|--------|-----------------|
| RESULT 9 | AR031572 | 131 bp | DNA | linear | PAT 29-SEP-1995 |
| LOCUS | AR031572 | | | | |
| DEFINITION | Sequence 11 from patent US 5866384. | | | | |
| ACCESSION | AR031572 | | | | |
| VERSION | AR031572.1 | GI:5945861 | | | |
| KEYWORDS | | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unknown. | | | | |

| REFERENCE | AUTHORS | TITLE | JOURNAL | FEATURES |
|--------------------|---|--|---------------------------------------|---------------------|
| Unclassified. | | | | |
| 1 (bases 1 to 131) | Hasseloff, J., Brand, A., Perlmutter, N. and Goodman, H.M | Cell ablation using trans-splicing ribozymes | Patent: US 5863384-A, 11-02-FEB-1999; | |
| | | | | Location/Qualifiers |
| | | | | 1..131 |

| | ORIGIN | |
|--------------------------|--------|---------------------------------|
| Query Match | 86.4% | Score 45.8; DB 6; Length 131; |
| Best Local Similarity | 95.9% | Pred. No. 4.6e-08; |
| Matches 47; Conservative | 0; | Mismatches 2; Indels 0; Gaps 0; |

| | |
|------------|-------------------------------------|
| RESULT | 10 |
| AR065684 | |
| LOCUS | AR065684 131 bp DNA |
| DEFINITION | Sequence 11 from patent US 5849548. |
| ACCESSION | AR065684 |
| VERSION | AR065684.1 GI:5995900 |

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REFERENCE          1 (bases 1 to 131)
AUTHORS            Haseloff,J.; Brand,A.; Perrimon,N. and Goodman,H.M
TITLE              Cell ablation using trans-splicing ribozymes
JOURNAL            Patent: US 5849548-A 11 15-DEC-1998;
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| Best Local Similarity | 95.9% | Pred. No. 4.6e-08 | | |
| Matches | 47 | Conservative | 0 | Mismatches 2, Indels 0, Gaps 0; |

| | | | |
|----|----|---|----|
| Oy | 1 | GATCCATGACAAATTCGATTCACCAACGCTGCTCGTAACCCGTCGAC | 49 |
| Db | 49 | GAGTCATGGAACAAATTCGATTCACCAACGCTGCTCGTAACCCGTCGAC | 97 |

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RESULT 11
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LOCUS AR097443 131 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6071730.
ACCESSION AR097443
VERSION AR097443.1 GI:12806173
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 11 06-JUN-2000;
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/mol_type="unassigned DNA"
ORIGIN

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| Query Match | 86.4% | Score | 45.8 | DB | 6 | Length | 131 |
| Best Local Similarly | 95.9% | Pred. NC | 4.6e-08 | | | | |
| Matches | 47 | Conservative | 0 | Mismatches | 2 | Indels | 0 |
| | | | | | | Gaps | 0 |

CC protein in a plant or plant cell by inserting a nucleic acid (NA)
CC encoding a ubiquitin monomer upstream of a NA encoding the desired
CC protein, where the fusion construct encodes a fusion protein and
CC expression is not controlled by the ubiquitin promoter. The invention
CC also relates to a NA acid vector a NA vector able to transform a plant
CC cell, that comprises NA encoding a fusion protein having a ubiquitin
CC monomer linked to a protein of interest and further, where expression of
CC the fusion construct is not under control of a ubiquitin promoter. The
CC construct allows enhanced production of the desired protein in plants or
CC plant cells

XX Sequence 53 BP; 15 A; 14 C; 13 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 53; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.9e-11;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GATCCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACGACT 53
1 GATCCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACGAGCT 53

RESULT 2

AAT34666 AAT34666 standard; DNA; 771 BP.

AC AAT34666;

DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)

DE Coat protein of the V34 strain of cucumber mosaic virus.

KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
resistance; ss.

XX Cucumber mosaic virus; strain V34.

XX Key Location/Qualifiers

FT CDS 3..659
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PN MO9621018-A1.

PD 11-JUL-1996.

PF 07-JUN-1995; 95WO-US007234.

PR 30-DEC-1994; 94US-00367789.

PA (ASGR-) ASGROW SEED CO.

PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

XX WPI; 1996-333993/33.

DR P-PSDB; AAR98895.

PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.

PS Claim 24; Fig 3; 80pp; English.

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 771 BP; 176 A; 199 C; 183 G; 213 T; 0 U; 0 Other;

Query Match 86.8%; Score 46; DB 2; Length 771;

Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 49
Db 1 CCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 46

RESULT 3

AAT34665 AAT34665 standard; DNA; 773 BP.

AC AAT34665;

DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)

DE Coat protein of the V33 strain of cucumber mosaic virus.

KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
resistance; ss.

XX Cucumber mosaic virus; strain V33.

XX Key Location/Qualifiers

FT CDS 3..659
/*tag= a

PN MO9621018-A1.

PD 11-JUL-1996.

PF 07-JUN-1995; 95WO-US007234.

PR 30-DEC-1994; 94US-00367789.

PA (ASGR-) ASGROW SEED CO.

PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

XX WPI; 1996-333993/33.

DR P-PSDB; AAR98894.

PT New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.

PS Claim 13; Fig 2; 80pp; English.

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 773 BP; 175 A; 200 C; 185 G; 213 T; 0 U; 0 Other;

Query Match 86.8%; Score 46; DB 2; Length 773;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 49
Db 1 CCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 46

RESULT 4

AAQ10461 AAQ10461 standard; cDNA; 976 BP.

AC AAQ10461;

```

DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-APR-1991 (first entry)
DE Capsid protein gene of Cucurbit Mosaic Virus strain FNY.
XX CMV, resistance; capsid protein; Cucumis melo; ss.
XX Cucurbit mosaic virus.
XX
XX Key Location/Qualifiers
XX CDS 75..731
XX /*tag= a
XX /product= "CMV strain FNY capsid protein"
XX
XX EP412912-A.
XX
XX 13-FEB-1991.
XX
XX 09-AUG-1990; 90EP-00402282.
XX
XX 11-AUG-1989; 89FR-00010848.
XX (BIOC-) BIOCEM SA.
XX
XX Deboth M, Bentahar S, Noel M, Perret J;
XX WPI; 1991-046027/07.
XX P-PSDB; AARI0652.
XX
XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
XX culture on specific medium for new transformed plants etc., esp.
XX resistant to cucumber mosaic virus.
XX
XX Claim 15; Page 17; 44pp; French.
XX
XX The gene was isolated from a plasmid (pUC18) containing DNA complementary
XX to RNA 3 of the virulent strain FNY, isolated in New York on infected
XX melons. The sequence includes a leader sequence, coding region and 3' non
XX -coding region. The leader sequence is the same length as that of the
XX Japanese Y strain of CMV. Transgenic melon plantlets containing the
XX sequence introduced via an Agrobacterium tumefaciens intermediate are
XX cultured as shoots in special media. The transformed melon plants are
XX resistant to CMV. See also AAQ10462. (Updated on 25-MAR-2003 to correct
XX PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX AUG-2003 to correct OS field.)
XX
XX Sequence 976 BP; 224 A; 249 C; 230 G; 273 T; 0 U; 0 Other;
SQ
Query Match 86.4%; Score 45.8; DB 2; Length 976;
Best Local Similarity 95.9%; Pred. No. 5.3e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GATCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 49
DB 70 GAGTCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 118
RESULT 5
AAQ10462
ID AAQ10462 standard; DNA; 1007 BP.
XX
XX AAQ10462;
XX
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 16-APR-1991 (first entry)
XX
XX Capsid protein gene of Cucurbit Mosaic Virus strain 117F.
XX CMV, resistance; capsid protein; Cucumis melo; ss.
XX
XX Cucurbit mosaic virus.
XX

```

```

XX Key Location/Qualifiers
XX CDS 54..710
XX /*tag= a
XX /product= "CMV strain 117F capsid protein"
XX
XX EP412912-A.
XX
XX 13-FEB-1991.
XX
XX 09-AUG-1990; 90EP-00402282.
XX
XX 11-AUG-1989; 89FR-00010848.
XX (BIOC-) BIOCEM SA.
XX
XX Deboth M, Bentahar S, Noel M, Perret J;
XX WPI; 1991-046027/07.
XX P-PSDB; AARI0653.
XX
XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
XX culture on specific medium for new transformed plants etc., esp.
XX resistant to cucumber mosaic virus.
XX
XX Claim 16; Page 19; 44pp; French.
XX
XX The gene was isolated from the virulent French strain 117F of CMV. Tomato
XX plantlets at the 2-leaf stage were infected with CMV strain 117F. 15 days
XX post-infection, the virus was purified from the infected leaves and cDNA
XX was synthesised from RNAs 1,2,3 and 4. After purification and selection
XX by standard techniques, cDNA complementary to RNA 4 was found to encode
XX the capsid protein. It was reinserted into "blue scribe" plasmids and
XX sequenced. Transgenic melon plantlets containing the sequence introduced
XX via an Agrobacterium tumefaciens intermediate are cultured as shoots in
XX special media. The transformed melon plants are resistant to CMV. See
XX also AAQ10461. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
XX 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
XX field.)
XX
XX Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;
SQ
Query Match 86.4%; Score 45.8; DB 2; Length 1007;
Best Local Similarity 95.9%; Pred. No. 5.4e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GATCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 49
DB 49 GAGTCATGACAAATCTGAATCAACCAAGTGTGTCGTAAACCGTCGACG 97
RESULT 6
AAQ67395
ID AAQ67395 standard; DNA; 1007 BP.
XX
XX AAQ67395;
XX
XX 25-MAR-2003 (revised)
XX 12-APR-1995 (first entry)
XX
XX Cauliflower mosaic virus capsid protein coding sequence.
XX
XX Cauliflower mosaic virus; CMV, capsid protein; coat protein;
XX polyribosome; inactive; inactivation; resistance; crop protection; ss.
XX
XX Cauliflower mosaic virus.
XX
XX Key Location/Qualifiers
XX CDS 54..710
XX /*tag= a
XX /product= "Capsid protein."
XX
XX FR2701960-A1.
XX

```

```

XX 02-SEP-1994.
PD 26-FEB-1993; 93FR-00002269.
PR 26-FEB-1993; 93FR-00002269.
XX 26-FEB-1993; 93FR-00002269.
XX (GENE-) GENE SHEARS PTY LTD.
XX
XX Lenae P, Perez P, Gruber V, Baudot G, Ollivo C;
DR WPI; 1994-281767/35.
DR P-PSDB; AAR57968.
XX
XX New polyribozyme contg. several catalytic regions in complementary
PT sequence - can inactivate gene for viral capsid protein, esp. for prepn.
PT of new virus resistant transgenic plants, also DNA sequence encoding it.
XX
XX Disclosure; Fig 2; 67pp; French.
XX
XX The RNA encoding the capsid protein of cauliflower mosaic virus can be
CC targeted by a nucleic acid sequence called a "polyribozyme". The
CC polyribozyme has endoribonuclease activity and is able to inactivate the
CC gene encoding the viral capsid protein. The polyribozyme comprises
CC several catalytic regions derived from ribozymes and confers complete
CC resistance to virus. See AAO67391-94. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
XX Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;
SQ
Query Match 86.4%; Score 45.8; DB 2; Length 1007;
Best Local Similarity 95.9%; Pred. No. 5.4e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GATCCATGACAAATCTGATATCAACCAAGTCTGCTGTAACCGTCGACG 49
DB 49 GAGTCATGACAAATCTGATATCAACCAAGTCTGCTGTAACCGTCGACG 97

```

RESULT 7
AAT99545/C
ID AAT99545 standard; cDNA; 1066 BP.

```

XX AAT99545;
AC
XX 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)
XX
XX Cucurbit mosaic virus RNA-3 cDNA fragment.
DE
XX Transgenic plant; virus resistance; disease resistance; RNA virus; CMV;
KW coat protein; antisense gene; ss.
XX
XX Cucurbit mosaic virus.
OS
XX Key Location/Qualifiers
FH 3'UTR 1..299
FT /tag= a
FT CDS 300..958
FT /tag= b
FT /product= "coat protein"
FT sig_peptide 956..1029
FT /tag= c
FT promoter /note= "coat protein leader sequence"
FT 1030..1066
FT /tag= d
FT /note= "F sequence of sub-genomic promoter"
XX
XX EP806481-A2.
XX 12-NOV-1997.
XX
XX 07-MAY-1997; 97EP-00201379.
XX

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XX 09-MAY-1996; 96IT-MI000927.
PR (META-) METAPONTUM AGROBIOS SCRL.
XX
XX Cellini F, Grieco PD;
XX
XX WPI; 1997-538620/50.
XX
XX Preparing transgenic plants resistant to RNA virus infection - using
PT anti:sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
XX Claim 3; Page 10; 18pp; English.
XX
XX This cDNA clone of cucumber mosaic virus (CMV) RNA-3 includes domain F of
CC the subgenomic promoter of viral RNA, the coat protein gene, its leader
CC sequence, and the tRNA-like 3'-terminal region of RNA-3. It was prepared
CC by amplifying a fragment of CMV cDNA-3 from clone PCR-CMV1RNA3 by PCR
CC (see also AAT99548-49). The gene construct is introduced into a vector
CC containing a promoter active in plant cells in antisense orientation
CC relative to the promoter. A claimed recombinant vector comprises the
CC plant promoter, the antisense gene construct and a terminator which is
CC functional in the plant. In addition to CMV, viral RNA may also be used
CC from tobacco mosaic virus and potato virus. Claimed transgenic plants
CC have the antisense gene construct integrated into their genomes. They are
CC resistant to viral infection. In particular, they are resistant to CMV.
CC Within the antisense gene construct, the interfering activity of the
CC antisense F domain of the sub-genomic promoter, associated with the
CC antisense activity performed by the coat protein gene, allows production
CC of plants having 100% resistance to CMV. (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
XX Sequence 1066 BP; 299 A; 251 C; 273 G; 243 T; 0 U; 0 Other;
SQ
Query Match 86.4%; Score 45.8; DB 2; Length 1066;
Best Local Similarity 95.9%; Pred. No. 5.4e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GATCCATGACAAATCTGATATCAACCAAGTCTGCTGTAACCGTCGACG 49
DB 961 GAGTCATGACAAATCTGATATCAACCAAGTCTGCTGTAACCGTCGACG 913

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RESULT 8
AAZ07505/C

```

XX AAZ07505;
AC
XX 26-NOV-1999 (first entry)
DT
XX
XX Cucurbit mosaic virus (CMV) RNA-3 gene cDNA clone fragment.
DE
XX Transgenic plant; RNA virus; antisense construct; cucumber mosaic virus;
KW CMV; promoter; coat protein gene; infection; RNA-3; ss.
XX
XX Cucurbit mosaic virus.
OS
XX US5959181-A.
XX
XX 28-SEP-1999.
PD
XX 09-MAY-1997; 97US-00854170.
XX
XX 09-MAY-1996; 96IT-MI000927.
XX
XX (META-) METAPONTUM AGROBIOS SCRL.
XX
XX Cellini F, Grieco PD;
XX
XX WPI; 1997-538620/50.
XX

```

PT Preparing transgenic plants resistant to RNA virus infection - using
PT anti-sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
PS Claim 2; Fig 1; 15pp; English.
XX
CC The invention relates to preparing transgenic plants resistant to RNA
CC virus induced infections that comprises integrating an antisense gene
CC construct into the plant genome. The construct comprises: (a) an P domain
CC of a subgenomic promoter of cucumber mosaic virus (CMV); (b) downstream
CC from the subgenomic promoter, a leader sequence of a coat protein gene of
CC CMV; (c) downstream from the leader sequence, a gene encoding a CMV coat
CC protein; and (d) downstream from the gene, a 3'-terminal region of a CMV
CC coat protein gene. The method is useful for producing plants which are
CC resistant to infection by RNA based viruses. The gene construct gives
CC higher levels of resistance compared to antisense constructs which are
CC capable of complementing with different domains of genomic RNA of CMV.
CC The present sequence represents the fragment of cDNA clone of RNA-3 of
CC CMV. This forms the antisense construct of the invention
XX
SQ Sequence 1067 BP; 297 A; 250 C; 276 G; 244 T; 0 U; 0 Other;
XX
Query Match 86.4%; Score 45.8; DB 2; Length 1067;
Best Local Similarity 95.9%; Pred. No. 5.4e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 GATCGATGACCAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 49
DB 961 GAGTCATGACCAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 913
XX
RESULT 9
ID AAN81111 standard; DNA; 1379 BP.
XX
AC AAN81111;
XX
DT 25-MAR-2003 (revised)
DT 12-NOV-1990 (first entry)
XX
DE Sequence contg. CMV strain Y coat protein gene.
XX
KM Cucumber mosaic virus; plant viral resistance; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH CDS 418..1074
FT /*tag= a
FT /label= cucumber mosaic virus-Y coat protein.
XX
FN EP279433-A.
XX
PD 24-AUG-1988.
XX
PF 18-FEB-1988; 88EP-00102322.
XX
PR 20-FEB-1987; 87JP-00038288.
PR 25-FEB-1987; 87JP-00043443.
PR 18-FEB-1988; 88JP-00035809.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Furusawa I, Onda H, Komiya T;
XX
XX WPI: 1988-236708/34.
DR P-PSDB; AAP80509.
XX
PT DNA coding for the coat protein of cucumber mosaic virus strain Y - used
PT for producing plants resistant to cucumber mosaic virus infection.
XX
PS Disclosure; Page 7; 20pp; English.
XX

CC This DNA is produced on screening of a plasmid library and is used to
CC transform plant cells which subsequently produce the coat prot- ein of
CC cucumber mosaic virus (CMV) strain Y. This protein is not synthesised in
CC natural plant cells. The resistance to CMV infect- ion, provided by the
CC DNA, is shown in plant cells and redifferent- iated plant bodies. See
CC also AAN81110. (Updated on 25-MAR-2003 to correct PR field.) (Updated on
CC 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1379 BP; 306 A; 342 C; 333 G; 398 T; 0 U; 0 Other;
XX
Query Match 86.4%; Score 45.8; DB 1; Length 1379;
Best Local Similarity 95.3%; Pred. No. 5.7e-08;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 GATCGATGACCAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 49
DB 413 GAGTCATGACCAATCTGAATCAACCACTGCTGCTGTAACCGTCGACG 461
XX
RESULT 10
ID AAQ76107 standard; DNA; 1696 BP.
XX
AC AAQ76107;
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE Cucumber mosaic virus RNA-3 chimera encoding RNase TI.
XX
KM Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KM virus resistance; disease resistance; transgenic plant; cross protection;
KM hypersensitive response; crop improvement; tomato;
KM Lycopersicon esculentum; tobacco; Nicotiana tabacum; RNase TI;
KM cell inhibitory protein; ToMV; CMV; ss.
XX
OS Cucumber mosaic virus.
XX
FH Key Location/Qualifiers
FH CDS 123..437
FT /*tag= a
FT /product= "RNase TI"
XX
FN W09429464-A1.
XX
PD 22-DEC-1994.
XX
PF 03-JUN-1994; 94MO-EP001817.
XX
PR 04-JUN-1993; 93GB-00011593.
XX
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI De Haan PT;
XX
XX WPI: 1995-036490/05.
DR P-PSDB; AAR67754.
XX
PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
PT encodes RNA that interacts with viral RNA polymerase to generate an
PT eliciting agent.
XX
XX Claim 4; Page 31-32; 50pp; English.
XX
XX A chimeric cucumber mosaic virus RNA-3 (given in AAQ76107) has the coat
XX protein gene replaced by a gene encoding a cell inhibitory protein, RNase
XX TI, having the sequence given in AAR67754. The construct elicits a minus-
XX sense RNA that interacts with the RNA-dependent RNA-polymerase of an
XX invading virus, thus conferring virus-resistance on a host plant, e.g.
XX tobacco, tomato. (Updated on 25-MAR-2003 to correct PN field.)
XX


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ID  AAT34664 standard; DNA; 772 BP.
XX
AC  AAT34664;
XX
DT  16-OCT-2003 (revised)
DT  02-DEC-1996 (first entry)
XX
DE  Coat protein of the V27 strain of cucumber mosaic virus.
XX
KM  Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
    resistance; ss.
XX
OS  Cucumber mosaic virus; strain V27.
XX
FH  Key      Location/Qualifiers
FT  CDS      3..659
          /*tag= a
XX
XX  MO9621018-A1.
XX
PD  11-JUL-1996.
XX
PF  07-JUN-1995; 95WO-US007234.
XX
PR  30-DEC-1994; 94US-00367789.
XX
PA  (ASGR-) ASGROW SEED CO.
XX
PI  Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
DR  WPI; 1996-333993/33.
DR  P-PSDB; AAR98893.
XX
FT  New isolated cucumber mosaic virus coat protein DNA - used to produce
PT  plants, partic. of the family Cucurbitaceae or Solanaceae, which are
    resistant to infection.
XX
PS  Claim 2; Fig 1; 80pp; English.
XX
CC  Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC  mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC  infected plant tissue by PCR amplification of cDNA using primers based on
CC  known CP sequences. The genes may be used for producing plants such as
CC  quash, cucumber, peppers and tomatoes which are resistant to CMV
CC  infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ  Sequence 772 BP; 177 A; 202 C; 182 G; 211 T; 0 U; 0 Other;

Query Match      83.8%; Score 44.4; DB 2; Length 772;
Best Local Similarity 97.8%; Pred. No. 1.8e-07;
Matches 45; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  4 CCATGACCAATCTGATCAACCAAGTCTGTCGTAAACCGTCGACG 49
    |||||
    1 CCATGACCAATCTGATCAACCAAGTCTGTCGTAAACCGTCGACG 46
DB

RESULT 14
AAT17259
ID  AAT17259 standard; DNA; 772 BP.
XX
AC  AAT17259;
XX
DT  16-OCT-2003 (revised)
DT  02-DEC-1996 (first entry)
XX
DE  Coat protein of the A35 strain of cucumber mosaic virus.
XX
KM  Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
    resistance; ss.
XX
OS  Cucumber mosaic virus; strain A35.
XX

```

```

FH  Key      Location/Qualifiers
FT  CDS      3..659
          /*tag= a
XX
XX  MO9621018-A1.
XX
PD  11-JUL-1996.
XX
PF  07-JUN-1995; 95WO-US007234.
XX
PR  30-DEC-1994; 94US-00367789.
XX
PA  (ASGR-) ASGROW SEED CO.
XX
PI  Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
DR  WPI; 1996-333993/33.
DR  P-PSDB; AAR93803.
XX
XX  New isolated cucumber mosaic virus coat protein DNA - used to produce
PT  plants, partic. of the family Cucurbitaceae or Solanaceae, which are
    resistant to infection.
XX
PS  Disclosure; Fig 8; 80pp; English.
XX
CC  Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC  mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC  infected plant tissue by PCR amplification of cDNA using primers based on
CC  known CP sequences. The genes may be used for producing plants such as
CC  quash, cucumber, peppers and tomatoes which are resistant to CMV
CC  infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ  Sequence 772 BP; 175 A; 201 C; 185 G; 211 T; 0 U; 0 Other;

Query Match      83.8%; Score 44.4; DB 2; Length 772;
Best Local Similarity 97.8%; Pred. No. 1.8e-07;
Matches 45; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  4 CCATGACCAATCTGATCAACCAAGTCTGTCGTAAACCGTCGACG 49
    |||||
    1 CCATGACCAATCTGATCAACCAAGTCTGTCGTAAACCGTCGACG 46
DB

RESULT 15
AAN90249
ID  AAN90249 standard; DNA; 1423 BP.
XX
AC  AAN90249;
XX
DT  24-OCT-2003 (revised)
DT  25-MAR-2003 (revised)
DT  01-NOV-1989 (first entry)
XX
DE  Cucumber mosaic virus C coat protein gene.
XX
KM  Cucumber mosaic virus C strain; virus-resistant plants; cucurbitacea;
    solanacea.
XX
OS  Cucumber mosaic virus; C strain.
XX
PN  MO8905858-A.
XX
PD  29-JUN-1989.
XX
PF  08-DEC-1988; 88WO-US004321.
XX
PR  21-DEC-1987; 87US-00135591.
XX
PA  (UPJO ) UPJOHN CO.
XX
PI  Quemada H, Slightom JL;
XX  WPI; 1989-206617/28.
XX

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XX Coat protein gene from C strain of cucumber mosaic virus - used to
PT prepare plant transformation vectors and virus-resistant plants.
XX
PS Claim 1; Page 15; 19pp; English.
XX
CC Coat protein gene from cucumber mosaic virus C strain is inserted into a
CC transformation vector also comprising the 35S promoter of cauliflower
CC mosaic virus, and the polyadenylation signal of either the CaMV 35S gene
CC or the Phaseolus vulgaris seed storage gene. This is used to transform
CC plants of cucurbitacea and solanacea to produce virus-resistant plants.
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 1423 BP; 385 A; 337 C; 320 G; 381 T; 0 U; 0 Other;
Query Match 83.4%; Score 44.2; DB 1; Length 1423;
Best Local Similarity 93.9%; Pred. No. 2.5e-07;
Matches 46; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 GATCCTGACCAATCTGAATCAACCACTGCTGTCGTAACCGTCGACG 49
Db 370 GAGTCATGACCAATCTGAATCAACCACTGCTGTCGTAACCGTCGACG 418

```

Search completed: December 5, 2004, 06:13:16
 Job time : 227 secs

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 03:35:58 ; Search time 1476 Seconds
(without alignments)
1308.473 Million cell updates/sec

Title: US-09-857-841-3

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Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Listing first 45 summaries

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| C 1 | 45.8 | 86.4 | 127 | 4 | BM067231 KS08001E1 |
| C 2 | 25.8 | 48.7 | 200 | 7 | H07817 kntj009 BNL |
| C 3 | 24.4 | 46.0 | 571 | 1 | AV589910 AV589910 |
| C 4 | 24.2 | 45.7 | 711 | 8 | CR153168 Forward B |
| C 5 | 24.2 | 45.7 | 807 | 8 | CC140418 ND1.2417. |
| C 6 | 24.2 | 45.7 | 1061 | 5 | BX376013 BX376013 |
| C 7 | 24.2 | 45.3 | 350 | 9 | CG880078 ZM88B050 |
| C 8 | 24.2 | 45.3 | 465 | 6 | CD122050 ME1-0070P |
| C 9 | 24.2 | 45.3 | 497 | 6 | CD121836 ME1-0070P |
| C 10 | 24.2 | 45.3 | 751 | 8 | AZ339011 1M070L18 |
| C 11 | 23.8 | 44.9 | 573 | 4 | BJ360440 387348 MA |
| C 12 | 23.8 | 44.9 | 573 | 4 | BJ360440 387348 MA |
| C 13 | 23.8 | 44.9 | 631 | 7 | BN967398 ES170 Tom |
| C 14 | 23.6 | 44.5 | 666 | 9 | CG815885 ZM88B052 |
| C 15 | 23.6 | 44.5 | 703 | 7 | CO703958 DG32-270K |
| C 16 | 23.6 | 44.5 | 772 | 9 | CG882815 ZM88B049 |
| C 17 | 23.6 | 44.5 | 952 | 9 | CG815885 ZM88B052 |
| C 18 | 23.6 | 44.5 | 952 | 9 | CG815885 ZM88B052 |
| C 19 | 23.6 | 44.5 | 952 | 9 | CG815885 ZM88B052 |
| C 20 | 23.4 | 44.2 | 372 | 5 | BM967398 ES170 Tom |
| C 21 | 23.4 | 44.2 | 409 | 2 | BE433697 EST40658 |
| C 22 | 23.4 | 44.2 | 447 | 2 | BE433697 EST40658 |
| C 23 | 23.4 | 44.2 | 448 | 2 | BE433697 EST40658 |
| C 24 | 23.4 | 44.2 | 471 | 8 | AO666369 HS_5367_B |

| | | | | | |
|------|------|------|-----|---|--------------------|
| C 25 | 23.4 | 44.2 | 494 | 2 | AW933614 EST359457 |
| C 26 | 23.4 | 44.2 | 507 | 2 | BE434784 EST405862 |
| C 27 | 23.4 | 44.2 | 509 | 2 | BE433535 EST400664 |
| C 28 | 23.4 | 44.2 | 525 | 2 | BE461053 EST412472 |
| C 29 | 23.4 | 44.2 | 539 | 2 | BE436288 EST407366 |
| C 30 | 23.4 | 44.2 | 544 | 2 | BE460657 EST412076 |
| C 31 | 23.4 | 44.2 | 567 | 2 | AW220906 EST293735 |
| C 32 | 23.4 | 44.2 | 569 | 2 | BE112783 EST440373 |
| C 33 | 23.4 | 44.2 | 570 | 2 | BE462001 EST413339 |
| C 34 | 23.4 | 44.2 | 571 | 2 | BE460690 EST412109 |
| C 35 | 23.4 | 44.2 | 596 | 2 | BE436895 EST408013 |
| C 36 | 23.4 | 44.2 | 607 | 2 | BE434904 EST405982 |
| C 37 | 23.4 | 44.2 | 612 | 2 | BE051011 EST436186 |
| C 38 | 23.4 | 44.2 | 614 | 2 | BE113438 EST441028 |
| C 39 | 23.4 | 44.2 | 617 | 2 | AW221834 EST298645 |
| C 40 | 23.4 | 44.2 | 627 | 8 | BE977843 Ode14C11. |
| C 41 | 23.4 | 44.2 | 629 | 2 | AW221911 EST298722 |
| C 42 | 23.4 | 44.2 | 632 | 2 | BE434157 EST405235 |
| C 43 | 23.4 | 44.2 | 642 | 2 | BE435313 EST406391 |
| C 44 | 23.4 | 44.2 | 667 | 2 | AW442094 EST311490 |
| C 45 | 23.4 | 44.2 | 674 | 2 | AW934244 EST360087 |

ALIGNMENTS

RESULT 1
BM067231/c 127 bp mRNA linear EST 11-SEP-2002
LOCUS BM067231 KS08001E12 KS08 Capsicum annuum cDNA, mRNA sequence.
DEFINITION BM067231
ACCESSION BM067231.1 GI:22787366
VERSION
KEYWORDS
SOURCE
ORGANISM
Capsicum annuum
Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Capsicum.

REFERENCE
AUTHORS
Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S.,
Hur, C.-G. and Choi, D.
Generation of Expressed Sequence Tags from Hot Pepper (Capsicum
annuum L.) and Sequence Analysis in Relation to Hypersensitive
Response Against Pathogen

JOURNAL
COMMENT
Contact: Doll Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4309
Fax: 82-42-860-4340
Email: dollchoi@kribb.re.kr

FEATURES
source
High quality sequence stop: 127.
Location/Qualifiers

1..127
/organism="Capsicum annuum"
/mol_type="mRNA"
/db_xref="taxon:4072"
/db_xref="taxon:4072"
/cdate="10 weeks after germination"
/clone_lib="KS08"
/note="Vector: pBluescript SK(-)"

ORIGIN

Query Match 86.4%; Score 45.8; DB 4; Length 127;
Best Local Similarity 95.9%; Pred. No. 3.4e-07;
Matches 47; Conservativity 0; Mismatches 2; Indels 0;

OY 1 GATCATGACAAATCGAATCAACAGTGTGCTGTAACCGTCGACG 49
DB 83 GATCATGACAAATCGAATCAACAGTGTGCTGTAACCGTCGACG 35

RESULT 2
LOCUS H07817/c 200 bp mRNA linear EST 23-JUN-1995
DEFINITION KhtJ009 BNL1 Brassica napus cDNA 3', mRNA sequence.
ACCESSION H07817
VERSION H07817.1 GI:872639
KEYWORDS EST.
SOURCE Brassica napus (rape)
ORGANISM Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 200)
Sohn,U., Lee,C.M., Cho,K.H., Jeon,Y.H., Hahn,T.R. and Nam,H.G.
CDNAs from Brassica napus (rape)
Unpublished (1995)
Other ESTs: Arabidopsis dbEST T44633
Contact: Uik Sohn
Laboratory of Molecular Biology
Kyunpook National University
Dept. of Genetic Eng., Kyunpook National Univ., Taegu 702-701, Korea
Tel.: 0539505382
Fax: 0539555327
Email: usohn@kh.kyunpook.ac.kr
EST is putatively homologous to Arabidopsis dbEST T44633
Seq primer: M13 forward
Location/Qualifiers
1..200
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Naehan"
/db_xref="taxon:3708"
/lab_host="NMS22"
/clone_lid="BNL1"
/note="Vector: pRTT3D; Site 1: NotI; Site 2: EcoRI; Poly(A)-mRNA was purified from the leaf of B.napus. cDNA library was constructed from the mRNAs by oligo(dT) priming and directionally cloned from the NotI site in the vector pRTT3D (Pharmacia) to the EcoRI site."

ORIGIN
Query Match 48.7%; Score 25.8; DB 7; Length 200;
Best Local Similarity 67.9%; Pred. No. 28;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 GATCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTGACGAGCT 53
DB 200 GATCAGACGCTCGATCGATCGAACCGTTGGTGTGTCACAGTCGACGATCT 148

RESULT 3
LOCUS AVS89910 571 bp mRNA linear EST 27-NOV-2001
DEFINITION AVS89910 Bos taurus brain fetus Bos taurus cDNA clone E1BR009C12
5', mRNA sequence.
ACCESSION AVS89910
VERSION AVS89910.1 GI:9700903
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 571)
Takauega,A., Hirotsune,S., Itoh,R., Jitchozono,A., Suzuki,H., Aso,H. and Sugimoto,Y.
Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs
Nucleic Acids Res. 29 (22), E108 (2001)
JOURNAL MEDLINE 21570554
PUBMED 11713328

COMMENT
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel.: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
1..571
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="E1BR009C12"
/tissue_type="brain"
/dev_stage="fetus"
/lab_host="DH10B"
/clone_lid="Bos taurus brain fetus"
/note="Vector: pZLI; Site 1: SalI; Site 2: NotI; Poly A was deleted from a NotI site"

ORIGIN
Query Match 46.0%; Score 24.4; DB 1; Length 571;
Best Local Similarity 73.8%; Pred. No. 1.2e+02;
Matches 31; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2 ATCCATGACAAATCTGAATCAACCACTGCTGCTGTAACCG 43
DB 264 ATCCATGACCAAGTGTACAAACCAAGCTGACGATGACGG 305

RESULT 4
LOCUS CR153168 711 bp DNA linear GSS 06-JUN-2004
DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN77n06, genomic survey sequence.
ACCESSION CR153168
VERSION CR153168.1 GI:49923013
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 711)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,D., Smith,D., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.
Direct Submision
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICR
Location/Qualifiers
1..711
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN77n06"
/clone_lid="MHPN"

ORIGIN
Query Match 45.7%; Score 24.2; DB 9; Length 711;
Best Local Similarity 71.1%; Pred. No. 1.4e+02;
Matches 32; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 2 ATCCATGACAAATCTGAATCAACCACTGCTGCTGTAACCGTGC 46
DB 585 ATATATGCTCATCTTAATTAACAGTGTGACCTTAACAGTTG 629

RESULT 5
LOCUS CC140418 807 bp DNA linear GSS 16-APR-2003
DEFINITION ND1.2417.SP6 Notre Dame Liverpool Nedes aegypti genomic clone

NDL.2417, genomic survey sequence.

ACCESSION CCI40418
VERSION CCI40418.1 GI:30009473

KEYWORDS GSS: Aedes aegypti (yellow fever mosquito)

SOURCE

Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes; Stegomyia.

1 (bases 1 to 807)

REFERENCE 1 (bases 1 to 807)
AUTHORS Loftus,B., Shetty,J., Knudson,D. and Severson,D.
TITLE BAC end sequencing of Aedes aegypti
JOURNAL Unpublished (2003)
COMMENT Other GSSs: NDL.2417.T7
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: SP6
Class: BAC ends.

FEATURES
source Location/Qualifiers

1..807
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="NDL.2417"
/note="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

ORIGIN

Query Match 45.7%; Score 24.2; DB 8; Length 807;
Best Local Similarity 71.1%; Pred. No. 1.5e+02;
Matches 32; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

2 ATCCATGACAAATCTGAATCAACACGCTGCTGTAACCGTCG 46
DB 559 AACCATGCTCACATTGTAATGACCCCATCTCTGTAACCGTCG 643

RESULT 6 BX376013 1061 bp mRNA linear EST 23-APR-2004
LOCUS BX376013 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION BX376013 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
ACCESSION BX376013
VERSION BX376013.2 GI:46555591
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1061)
Li,W.B., Gruber,C., Jessee,J. and Polayer,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30434740.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr

REFERENCE 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster

2789.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdnars-CS0DC021AG06NP1&c=2789.f.

FEATURES

source Location/Qualifiers

1..1061
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC021YM11"
/rissue="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 45.7%; Score 24.2; DB 5; Length 1061;
Best Local Similarity 61.7%; Pred. No. 1.5e+02;
Matches 29; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 GATCCATGACAAATCTGAATCAACACGCTGCTGTAACCGTCGA 47
DB 1009 GATCCTTGCCCMMTGAGATGATCATTCATGCTGCTCATCCAMGA 1055

RESULT 7 CG880078 350 bp DNA linear GSS 02-DEC-2003
LOCUS CG880078 ZMMBB0504M22 ZMMBB (HindIII) Zea mays genomic clone
DEFINITION ZMMBB0504M22 5', genomic survey sequence.
ACCESSION CG880078
VERSION CG880078.1 GI:38610691
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 350)
Bharti,A.K., Young,S., Kaychok,S., Keizer,G., Bronzino,A.C., Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PCR (2003c)
Unpublished (2003)
Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 85.

FEATURES
source Location/Qualifiers

1..350
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBB0504M22"
/lab_host="E. coli DH108"
/clone_lib="ZMMBB (HindIII)"
/note="Vector: pCUG1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 45.3%; Score 24; DB 9; Length 350;
Best Local Similarity 68.8%; Pred. No. 1.5e+02;
Matches 33; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 ATCCATGACAAATCTGAATCAACACGCTGCTGTAACCGTCGACG 49
|||||

Db 337 ATCAATGACAAATTGTAATTAACCGTTCTTTTCATCGTCGTCG 290

RESULT 8
CD122050 465 bp mRNA linear EST 14-SEP-2003

LOCUS
DEFINITION MEI-0070P-V208-H01-U.B MEI-0070 Schistosoma mansoni CDNA clone

ACCESSION
VERSION CD122050
KEYWORDS CD122050.1 GI:34660102

SOURCE
ORGANISM Schistosoma mansoni
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigidae; Schistosomatidae; Schistosomatidae; Schistosoma.

REFERENCE
AUTHORS Verjovski-Almeida, S., Demarco, R., Martins, E.A.L., Guimaraes, P.E.M.,
Ojopi, E.P.B., Paquola, A.C.M., Plazza, J.P., Nishiyama, M.Y., Jr.,
Kiteajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,
Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,
Lette, R.A., Malaguas, L.C.C., Marques, R.C.P., Miyasato, P.A.,
Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,
Secubal, J.C., Leite, L.C.C. and Dias-Neto, E.
Transcriptome analysis of the acelomate human parasite Schistosoma
mansoni
Nat. Genet. 35 (2), 148-157 (2003)

JOURNAL
MEDLINE 22879926
PubMed 12973350

COMMENT
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Departamento de Bioquímica
Instituto de Química - Universidade de São Paulo
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Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjowski@usp.br
This sequence was derived from the PAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL: <http://bioinfo.iq.usp.br/schisto/>
Plate: MEI-0070P-V208 row: 1 column: H.

FEATURES
source
1..465
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="MEI-0070P-V208-H01.B"
/sex="mixed pool"
/dev_stage="egg"
/lab_host="Mus musculus"
/clone_lib="MEI-0070"
/note="Vector: pGEM T-easy"

ORIGIN
Query Match 45.3%; Score 24; DB 6; Length 465;
Best Local Similarity 68.8%; Pred. No. 1.6e+02;
Matches 33; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 267 ACCATGACAAATCTGAATCAACGAGTGTGTAACCGTCGACG 49

RESULT 9
CD121836 497 bp mRNA linear EST 14-SEP-2003

LOCUS
DEFINITION MEI-0070P-V169-C07-U.B MEI-0070 Schistosoma mansoni CDNA clone

ACCESSION
VERSION CD121836
KEYWORDS CD121836.1 GI:34659890

SOURCE
ORGANISM Schistosoma mansoni
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigidae; Schistosomatidae; Schistosomatidae; Schistosoma.

REFERENCE
AUTHORS Verjovski-Almeida, S., Demarco, R., Martins, E.A.L., Guimaraes, P.E.M.,
Ojopi, E.P.B., Paquola, A.C.M., Plazza, J.P., Nishiyama, M.Y., Jr.,
Kiteajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,
Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,
Lette, R.A., Malaguas, L.C.C., Marques, R.C.P., Miyasato, P.A.,
Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,
Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,
Secubal, J.C., Leite, L.C.C. and Dias-Neto, E.
Transcriptome analysis of the acelomate human parasite Schistosoma
mansoni
Nat. Genet. 35 (2), 148-157 (2003)

JOURNAL
MEDLINE 22879926
PubMed 12973350

COMMENT
Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquímica
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Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP,
Brasil
Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjowski@usp.br
This sequence was derived from the PAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL: <http://bioinfo.iq.usp.br/schisto/>
Plate: MEI-0070P-V169 row: 7 column: C.

FEATURES
source
1..497
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="MEI-0070P-V169-C07.B"
/sex="mixed pool"
/dev_stage="egg"
/lab_host="Mus musculus"
/clone_lib="MEI-0070"
/note="Vector: pGEM T-easy"

ORIGIN
Query Match 45.3%; Score 24; DB 6; Length 497;
Best Local Similarity 68.8%; Pred. No. 1.6e+02;
Matches 33; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 267 ACCATGACAAATCTGAATCAACGAGTGTGTAACCGTCGACG 49

RESULT 10
A2339011 751 bp DNA linear GSS 29-SEP-2000

LOCUS
DEFINITION IM0070L1F Mouse 10kb plasmid UGCM library Mus musculus genomic
clone UGCM0070L1F F, genomic survey sequence.

ACCESSION
VERSION A2339011
KEYWORDS A2339011.1 GI:10412854

SOURCE
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0070 Row: L Column: 18
Seq primer: CATTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 751.
Location/Qualifiers

FEATURES

source

1..751
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0070L18"
/sex="Male"
/lab_host="B. Coi strain X110-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor-competent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 45.3%; Score 24; DB 8; Length 751;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 5 CATGACAAATCTGATCAACGCTGCTGCTAACCGT 44
Db 50 CATGACTAATCTGAATGAAGACGACTTGCCATCACCCT 89

RESULT 11

Bj232993/c

LOCUS Bj232993 417 bp mRNA linear EST 05-APR-2002
DEFINITION Bj232993 Y. Ogihara unpublished cDNA library, wh_e Triticum
aestivum cDNA clone whe2005 5', mRNA sequence.

ACCESSION Bj232993
VERSION Bj232993.1 GI:20050477
KEYWORDS EST
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

1 (bases 1 to 417)

Ogihara, Y. and Murai, K.

Expressed genes in Triticum aestivum
Unpublished (2002)

REFERENCE
CONTACT: Tadasu Shin-i
Center For Genetic Resource Information

National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsbini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES

source

1..417
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whe2005"
/tissue_type="seed DPA10"
/dev_stage="Peekes' scale 11.2"
/clone_lib="Y. Ogihara unpublished cDNA library, wh_e"

ORIGIN

Query Match 44.9%; Score 23.8; DB 4; Length 417;
Best Local Similarity 65.4%; Pred. No. 1.9e+02;
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 2 ATCCATGGACAATCTGATCAACCACTGCTGCTGCTGACCTGAGAGCT 53
Db 394 ACCAGTTGAACACATCTGATCAACCTGAGCTGCTGCTGCTGCGCGAGCT 343

RESULT 12

Bj360440

LOCUS Bj360440 573 bp mRNA linear EST 01-AUG-2001
DEFINITION Bj37348 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.

ACCESSION Bj360440
VERSION Bj360440.1 GI:15056468
KEYWORDS EST

ORIGIN

source

Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 573)
Fahrenkrug, S.C., Smith, T.P.L., Preking, B.A., Cho, J., White, J.,
Vallet, J., Wise, T., Rohrer, G.A., Petree, G., Sultana, R.,
Quackenbush, J. and Keele, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)

REFERENCE

AUTHORS

TITLE

JOURNAL 22213789
MEDLINE 12226715
PubMed 12226715
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4356
Fax: 402 762 4350
Email: smith@meat.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.

COMMENT

PCR primers
FORWARD: AGGAACAAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 138 Row: A Column: 5
Seq primer: ATTAGGTCACACTATAG.
Location/Qualifiers

FEATURES

source

1..573
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2P1G"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

ORIGIN

Query Match 44.9%; Score 23.8; DB 4; Length 573;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 3 TCCATTGCAAAATCTGATCAACCGTGTGCTGCTAACCCTCCAGCGACT 53
52 TCCATTGCAAAAGAGAGACGCGAGTGTGTGCTGAGACAGTAAAGAGGT 102

Db 74 TCCATTGCAAAAGAGAGACGCGAGTGTGTGCTGAGACAGTAAAGAGGT 124

RESULT 13
EX922152 609 bp mRNA linear EST 22-JAN-2004
LOCUS BX922152 Sus scrofa library (scan) Sus scrofa cDNA clone
DEFINITION scan0022d.e.22 Sprim, mRNA sequence.
ACCESSION BX922152
VERSION BX922152
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 609)
AUTHORS Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S.,
Soares,M., Bonaldi,F. and Haley,F.
TITLE A Pig Normalised Multi-Tissue cDNA Library
JOURNAL Unpublished (2003)
COMMENT Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin du Borge-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Clone distribution: AGENAS Resource centre, Francois PIMU,
Francis.Pimu@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du
genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,
FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signanauporte@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0022 row: e column: 22.
Location/Qualifiers
1..609
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scan0022d.e.22"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
/clone_lib="Sus Scrofa library (scan)"
/note="Tissues: adipose tissue, brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenal, bulbo urethral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"

FEATURES
source
Location/Qualifiers
1..609
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scan0022d.e.22"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
/clone_lib="Sus Scrofa library (scan)"
/note="Tissues: adipose tissue, brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenal, bulbo urethral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"

ORIGIN
Query Match 44.9%; Score 23.8; DB 5; Length 609;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 3 TCCATTGCAAAATCTGATCAACCGTGTGCTGCTAACCCTCCAGCGACT 53
74 TCCATTGCAAAAGAGAGACGCGAGTGTGTGCTGAGACAGTAAAGAGGT 124

RESULT 14
LOCUS CN698549 631 bp mRNA linear EST 18-MAY-2004
DEFINITION E0409C12-5 NIA Mouse E11.5 whole embryo cDNA library (Long) Mus

musculus cDNA clone NIA:E0409C12 IMAGE:30869411 5', mRNA sequence.
CN698549
VERSION CN698549.1 GI:47467238
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 631)
AUTHORS Sharov,A.A., Piao,Y., Macoba,R., Dudekula,D.B., Qian,Y.,
VanBuren,V., Falco,G., Martin,P.R., Steag,C.A., Basey,U.C.,
Wang,Y., Carter,M.G., Hamatani,T., Albe,K., Akutsu,H., Sharova,L.,
Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
Nagaraja,R., Boheler,K.R., Raub,D., Hodges,R.J., Longo,D.L.,
Schlesinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
Vescovi,A.L., Rosant,J., Kunath,T., Hogan,B.L., Curci,A.,
D'Urso,M., Kelso,J., Hyde,W. and Ko,M.S.
TITLE Transcription analysis of mouse stem cells and early embryos
JOURNAL PLOS Biol. 1 (3), 410-419 (2003)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.igr.nia.nih.gov
Plate: E0409 row: C column: 12
Seq primer: M13 Reverse
High quality sequence stop: 631
POLY-A-NO.

FEATURES
source
Location/Qualifiers
1..631
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="nia:EST:E0409C12-5"
/db_xref="taxon:10090"
/clone="NIA:E0409C12 IMAGE:30869411"
/tissue_type="whole embryo including extraembryonic
tissues at 11.5-days postcoitum"
/dev_stage="E11.5"
/lab_host="DH10B"
/clone_lib="NIA Mouse E11.5 whole embryo cDNA library
(Long)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site:1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://1gsun.igr.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001)). [PMID: 11544191]. Total
RNAs were extracted from a pool of 3 embryos at 11.5-days
postcoitum. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer [Invitrogen:
5'-pGACTAGTCTGATCGAGCGCGCCCTTTT-TTTT-3'] from
2ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker L1-SalI, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer SalI-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 3.3kb. The library was
constructed by Yulan Piao."

ORIGIN
Query Match 44.5%; Score 23.6; DB 7; Length 631;
Best Local Similarity 69.6%; Pred. No. 2.4e+02;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 7 TGGCAAAATCTGATCAACCGTGTGCTGCTAACCCTCCAGCGAC 52

Db 354 TGACAAAGTGAAGACACCGTGTGCTGACCTTAACCTCACCCTGGC 399

RESULT 15

CL708124 666 bp DNA linear GSS 26-JUL-2004

LOCUS OR_BBa0028C18.r OR_BBa Oryza rufipogon genomic clone OR_BBa0028C18

DEFINITION 3' genomic survey sequence.

ACCESSION CL708124 GI:50595162

VERSION CL708124.1

KEYWORDS GSS.

SOURCE Oryza rufipogon

ORGANISM Oryza rufipogon Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 666)

AUTHORS Kim,H., Yu,Y., Stum,D., Yeat,D., Rao,K., Luo,M., Jetty,R.,

Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.

TITLE OMAP Project

JOURNAL Unpublished (2004)

COMMENT Contact: Rod A. Wing

Arizona Genomics Institute

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: <http://genome.arizona.edu>

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG

BACKWARD: CAC TCA TTA GGC ACC CCA

Insert Length: 161 Std Error: 0.00

Plate: 0028 row: C column: 18

Seq primer: CAC TCA TTA GGC ACC CCA

Class: BAC ends.

FEATURES

source 1..666

Location/Qualifiers

/organism="Oryza rufipogon"

/mol_type="genomic DNA"

/db_xref="taxon:4529"

/clone="OR_BBa0028C18"

/tissue_type="Young leaves"

/lab_host="DH10B-T1 phage resistant"

/clone_lib="OR_BBa"

/note="Vector: pGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 44.5% Score 23.6; DB 9; Length 666;

Best Local Similarity 76.3% Pred. No. 2.5e+02;

Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 10 ACAATCTGAATCAACAGTGTGCTGTAACCGTGA 47

DB 459 AAAAATTTTAATCCACAACGCTGCTGTAACCGATGA 496

Search completed: December 5, 2004, 06:38:00

Job time : 1480 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 08:16:57 ; Search time 2543 Seconds

(without alignments)
260.344 Million cell updates/sec

Title: US-09-857-841-4

Sequence: 1 MDKSESTSGAGNRR 14

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-Q=/cgn2.1/USPTO_epool/US09857841/runat_03122004_160551_18585/app_query.fasta.1.199
-DB=genEmbl -QEMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=ptc -NORM=ext -HEAPSIZE=500 -MTLEN=0 -MAXLEN=200000000
-USER=US09857841@cgn2.1 13731@runat_03122004_160551_18585 -NCPU=6 -ICPU=3
-NO MAP -LARGEOQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_srs:*
12: gb_sy:*
13: gb_un:*
14: gb_yi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 69 | 100.0 | 53 | 6 | BD261798 |
| 2 | 69 | 100.0 | 130 | 6 | BD261798 Enhanceme |
| 3 | 69 | 100.0 | 130 | 6 | AR031575 Sequence |
| 4 | 69 | 100.0 | 130 | 6 | AR065687 Sequence |
| | | | | | AR097446 Sequence |

| | | | | | | |
|----|----|-------|-----|----|----------|-------------|
| 5 | 69 | 100.0 | 130 | 6 | 149964 | Sequence 14 |
| 6 | 69 | 100.0 | 131 | 6 | AR031572 | Sequence |
| 7 | 69 | 100.0 | 131 | 6 | AR065684 | Sequence |
| 8 | 69 | 100.0 | 131 | 6 | AR097443 | Sequence |
| 9 | 69 | 100.0 | 131 | 6 | AR097443 | Sequence |
| 10 | 69 | 100.0 | 152 | 6 | AR031570 | Sequence |
| 11 | 69 | 100.0 | 152 | 6 | AR031571 | Sequence |
| 12 | 69 | 100.0 | 152 | 6 | AR065682 | Sequence |
| 13 | 69 | 100.0 | 152 | 6 | AR065683 | Sequence |
| 14 | 69 | 100.0 | 152 | 6 | AR097441 | Sequence |
| 15 | 69 | 100.0 | 152 | 6 | AR097442 | Sequence |
| 16 | 69 | 100.0 | 152 | 6 | 149959 | Sequence 9 |
| 17 | 69 | 100.0 | 152 | 6 | 149960 | Sequence 10 |
| 18 | 69 | 100.0 | 154 | 6 | AR031573 | Sequence |
| 19 | 69 | 100.0 | 154 | 6 | AR031574 | Sequence |
| 20 | 69 | 100.0 | 154 | 6 | AR065685 | Sequence |
| 21 | 69 | 100.0 | 154 | 6 | AR065686 | Sequence |
| 22 | 69 | 100.0 | 154 | 6 | AR097444 | Sequence |
| 23 | 69 | 100.0 | 154 | 6 | AR097445 | Sequence |
| 24 | 69 | 100.0 | 154 | 6 | 149962 | Sequence 12 |
| 25 | 69 | 100.0 | 154 | 6 | 149963 | Sequence 13 |
| 26 | 69 | 100.0 | 654 | 6 | B01760 | DNA encodin |
| 27 | 69 | 100.0 | 654 | 14 | AF444252 | Banana mo |
| 28 | 69 | 100.0 | 657 | 14 | AB070622 | Cucumber |
| 29 | 69 | 100.0 | 657 | 14 | AB109909 | Cucumber |
| 30 | 69 | 100.0 | 657 | 14 | AF198622 | Cucumber |
| 31 | 69 | 100.0 | 657 | 14 | AF198622 | Cucumber |
| 32 | 69 | 100.0 | 657 | 14 | AF316362 | Cucumber |
| 33 | 69 | 100.0 | 657 | 14 | AF350450 | Cucumber |
| 34 | 69 | 100.0 | 657 | 14 | AF368192 | Cucumber |
| 35 | 69 | 100.0 | 657 | 14 | AF523339 | Cucumber |
| 36 | 69 | 100.0 | 657 | 14 | AF523340 | Cucumber |
| 37 | 69 | 100.0 | 657 | 14 | AF523341 | Cucumber |
| 38 | 69 | 100.0 | 657 | 14 | AF523342 | Cucumber |
| 39 | 69 | 100.0 | 657 | 14 | AF523343 | Cucumber |
| 40 | 69 | 100.0 | 657 | 14 | AF523344 | Cucumber |
| 41 | 69 | 100.0 | 657 | 14 | AF523345 | Cucumber |
| 42 | 69 | 100.0 | 657 | 14 | AF523346 | Cucumber |
| 43 | 69 | 100.0 | 657 | 14 | AF523347 | Cucumber |
| 44 | 69 | 100.0 | 657 | 14 | AF523348 | Cucumber |
| 45 | 69 | 100.0 | 657 | 14 | AF523349 | Cucumber |

ALIGNMENTS

RESULT 1
BD261798
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD261798 53 bp DNA linear PAT 17-JUL-2003
Enhancement in protein production by higher plants using ubiquitin
or cucumber mosaic virus coating protein peptide.

BD261798.1 GI:33071566
JP 2002532098-A/2.
Cucumber mosaic virus (cucumber mosaic cucumovirus)
Cucumber mosaic virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
Cucumovirus.
1 (bases 1 to 53)
Fang,R.X., Wu,J.L. and Chen,X.Y.
Enhancement in protein production by higher plants using ubiquitin
or cucumber mosaic virus coating protein peptide
Patent: JP 2002532098-A 2 02-OCT-2002;
INSTITUTE OF MOLECULAR AGRICULTURE

OS Cucumber mosaic virus
PN JP 2002532098-A/2
PD 02-OCT-2002
PF 11-DEC-1998 JP 2000588378
PI RONG XIANG FANG JING LIN WU XIAO YING CHEN
PC C12N15/09,A01H5/00,C07K14/415,C07K19/00,C12N5/10,C12N5/00, PC
C12N5/00
CC Enhancement in protein production by higher plants using CC
ubiquitin or
CC cucumber mosaic virus coating protein peptide FH Key

Location/Qualifiers
(6). (47).
FEATURES FT CDS Location/Qualifiers
source 1..53
/organism="Cucumber mosaic virus"
/mol_type="genomic DNA"
/db_xref="taxon:12305"
ORIGIN

Alignment Scores:
Pred. No.: 0.000526 Length: 53
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x BD261798 (1-53)

OY 1 MetApLySeRgiUseRThSeRAlaGlyARgaAnARgArg 14
|||||
6 ATGGACAAATCTGATCAACCAAGTGTGCTGTACCGTCGA 47
|||||

RESULT 2
AR031575 130 bp DNA linear PAT 29-SEP-1999
LOCUS AR031575
DEFINITION Sequence 14 from patent US 5866384.
ACCESSION AR031575
VERSION AR031575.1 GI:5945864
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 14 02-FEB-1999;
FEATURES Location/Qualifiers
source 1..130
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 0.00137 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR031575 (1-130)

OY 1 MetApLySeRgiUseRThSeRAlaGlyARgaAnARgArg 14
|||||
53 ATGGACAAATCTGATCAACCAAGTGTGCTGTACCGTCGA 94
|||||

RESULT 3
AR065687 130 bp DNA linear PAT 29-SEP-1999
LOCUS AR065687
DEFINITION Sequence 14 from patent US 5849548.
ACCESSION AR065687
VERSION AR065687.1 GI:5995903
KEYWORDS
SOURCE Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 14 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..130

/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.: 0.00137 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR065687 (1-130)

OY 1 MetApLySeRgiUseRThSeRAlaGlyARgaAnARgArg 14
|||||
53 ATGGACAAATCTGATCAACCAAGTGTGCTGTACCGTCGA 94
|||||

RESULT 4
AR097446 130 bp DNA linear PAT 14-FEB-2001
LOCUS AR097446
DEFINITION Sequence 14 from patent US 6071730.
ACCESSION AR097446
VERSION AR097446.1 GI:12806176
KEYWORDS
SOURCE Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 14 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..130
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 0.00137 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR097446 (1-130)

OY 1 MetApLySeRgiUseRThSeRAlaGlyARgaAnARgArg 14
|||||
53 ATGGACAAATCTGATCAACCAAGTGTGCTGTACCGTCGA 94
|||||

RESULT 5
I49964 130 bp DNA linear PAT 07-OCT-1997
LOCUS I49964
DEFINITION Sequence 14 from patent US 5641673.
ACCESSION I49964
VERSION I49964.1 GI:2472184
KEYWORDS
SOURCE Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5641673-A 14 24-JUN-1997;
FEATURES Location/Qualifiers
source 1..130
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 0.00137 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x I49964 (1-130)

OY 1 MetApLySeRgUSeRThSeRAlaGlyArGaSaMaRgArG 14
DB 53 ATGGACAAATCTGAATCAACCAAGTCTGCTGTACCGTCGA 94

RESULT 6
LOCUS AR031572 131 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5866384.
ACCESSION AR031572
VERSION AR031572.1 GI:5945861
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 11 02-FEB-1999;
FEATURES Location/Qualifiers
source 1..131
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 0.00138 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR031572 (1-131)

OY 1 MetApLySeRgUSeRThSeRAlaGlyArGaSaMaRgArG 14
DB 54 ATGGACAAATCTGAATCAACCAAGTCTGCTGTACCGTCGA 95

RESULT 7
LOCUS AR065684 131 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5849548.
ACCESSION AR065684
VERSION AR065684.1 GI:5995900
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 11 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..131
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 0.00138 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR065684 (1-131)

OY 1 MetApLySeRgUSeRThSeRAlaGlyArGaSaMaRgArG 14
DB 54 ATGGACAAATCTGAATCAACCAAGTCTGCTGTACCGTCGA 95

RESULT 8
LOCUS AR097443 131 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6071730.
ACCESSION AR097443
VERSION AR097443.1 GI:12806173
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 11 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..131
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 0.00138 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR097443 (1-131)

OY 1 MetApLySeRgUSeRThSeRAlaGlyArGaSaMaRgArG 14
DB 54 ATGGACAAATCTGAATCAACCAAGTCTGCTGTACCGTCGA 95

RESULT 9
LOCUS I49961 131 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 11 from patent US 5641673.
ACCESSION I49961
VERSION I49961.1 GI:2472181
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5641673-A 11 24-JUN-1997;
FEATURES Location/Qualifiers
source 1..131
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 0.00138 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x I49961 (1-131)

OY 1 MetApLySeRgUSeRThSeRAlaGlyArGaSaMaRgArG 14

Db 54 ATGACAAATCTGAATCAACCAAGTCTGCTCTTAACCGTCGA 95
RESULT 10
LOCUS AR031570 152 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5866384.
ACCESSION AR031570
VERSION AR031570.1 GI:5945859
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 9 02-FEB-1999;
FEATURES
Location/Qualifiers
1..152
/organism="unknown"
/mol_type="unassigned DNA"

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Pred. No.: 0.00162 Length: 152
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-857-841-4 (1-14) x AR031571 (1-152)

OY 1 MetApLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 75 ATGACAAATCTGAATCAACCAAGTCTGCTCTTAACCGTCGA 116
RESULT 11
LOCUS AR031571 152 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5866384.
ACCESSION AR031571
VERSION AR031571.1 GI:5945860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 10 02-FEB-1999;
FEATURES
Location/Qualifiers
1..152
/organism="unknown"
/mol_type="unassigned DNA"

ALIGNMENT Scores:
Pred. No.: 0.00162 Length: 152
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-857-841-4 (1-14) x AR031571 (1-152)

OY 1 MetApLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 75 ATGACAAATCTGAATCAACCAAGTCTGCTCTTAACCGTCGA 116
RESULT 12
LOCUS AR065682 152 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5849548.
ACCESSION AR065682
VERSION AR065682.1 GI:5995898
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 9 15-DEC-1998;
FEATURES
Location/Qualifiers
1..152
/organism="unknown"
/mol_type="unassigned DNA"

ALIGNMENT Scores:
Pred. No.: 0.00162 Length: 152
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-857-841-4 (1-14) x AR065683 (1-152)

OY 1 MetApLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 75 ATGACAAATCTGAATCAACCAAGTCTGCTCTTAACCGTCGA 116
RESULT 13
LOCUS AR065683 152 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5849548.
ACCESSION AR065683
VERSION AR065683.1 GI:5995899
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 10 15-DEC-1998;
FEATURES
Location/Qualifiers
1..152
/organism="unknown"
/mol_type="unassigned DNA"

ALIGNMENT Scores:
Pred. No.: 0.00162 Length: 152
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-857-841-4 (1-14) x AR065683 (1-152)

OY 1 MetApLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 75 ATGACAAATCTGAATCAACCAAGTCTGCTCTTAACCGTCGA 116
RESULT 14
LOCUS AR097441 152 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6071730.
ACCESSION AR097441
VERSION AR097441.1 GI:12806171
KEYWORDS

| | |
|-----------|---|
| SOURCE | Unknown. |
| ORGANISM | Unknown. |
| REFERENCE | Unclassified. |
| AUTHORS | 1 (bases 1 to 152) |
| TITLE | Hasegawa, J., Brand, A., Perrimon, N. and Goodman, H.M. |
| JOURNAL | Cell ablation using trans-splicing ribozymes |
| FEATURES | Patent: US 6071730 A 9 06-JUN-2000; |
| SOURCE | Location/Qualifiers |
| | 1..152 |

| ORIGIN | |
|------------------------|---------|
| Alignment Scores: | |
| Pred. No.: | 0.00162 |
| Score: | 69.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 100.00% |
| DB: | 6 |
| | |
| Length: | 152 |
| Matches: | 14 |
| Conservative: | 0 |
| Mismatches: | 0 |
| Indels: | 0 |
| Gaps: | 0 |

US-09-857-841-4 (1-14) X AR097441 (1-152)

QY 1 MetAspIysSerGIuSerThrSerAlaGlyArgAsnArgArg 14
|||
Db 75 ATGACCAATCTGAATCAACGAGTGTGCTGTAACCGTGA 116

RESULT 15
AB007443

| | | | | |
|------------|-------------------------------------|-------------|-----|-----------------|
| LOCUS | AR097442 | 152 bp | DNA | PAT 14-FEB-2001 |
| DEFINITION | Sequence 10 from patent US 6071730. | | | |
| ACCESSION | AR097442 | | | |
| VERSION | AR097442.1 | GI:12806172 | | |

ORIGIN

| | |
|------------------------|---------|
| Alignment Scores: | |
| Pred. No.: | 0.00162 |
| Score: | 69.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 100.00% |
| DB: | 6 |
| | |
| Length: | 152 |
| Matches: | 14 |
| Conservative: | 0 |
| Mismatches: | 0 |
| Indels: | 0 |
| Gaps: | 0 |

US-09-857-841-4 (1-14) X AR097442 (1-152)

QY 1 MetAspIysSerGluSerThrSerAlaGlyArgAsnArgArg 14
DB 75 ATGATTAATCTGAATCAACCAAGTGGTGGTAAACGTCGA 116

Search completed: December 5, 2004, 09:07:02
Job time : 2544 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frama_plus_p2n model

Run on: December 5, 2004, 08:15:22 ; Search time 326 Seconds

(without alignments)
225.435 Million cell updates/sec

Title: US-09-857-841-4

Sequence: 1 MDKSESTAGRNRR 14

Scoring table:

| | |
|---------------------------|--|
| BLOSUM62 | |
| Xgapop 10.0 , Xgapext 0.5 | |
| Ygapop 10.0 , Ygapext 0.5 | |
| Fgapop 6.0 , Fgapext 7.0 | |
| Delop 6.0 , Delext 7.0 | |

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPRO.epool/US09857841/runat_03122004_160551_18575/app_query.fasta.1.199
-DB=N_Geneseq_23Sep04 -QMT=fastrap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US09857841 @CGN_1_1_470 @runat_03122004_160551_18575 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOUFRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N_Geneseq_23Sep04: *
1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
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6: geneseqn2002as: *
7: geneseqn2002bs: *
8: geneseqn2003as: *
9: geneseqn2003bs: *
10: geneseqn2003cs: *
11: geneseqn2003ds: *
12: geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|-------------|
| 1 | 69 | 100.0 | 53 | AAA30858 | Ubiquitin |
| 2 | 69 | 100.0 | 771 | AAT34666 | Coat prot |
| 3 | 69 | 100.0 | 772 | AAT34664 | Coat prot |
| 4 | 69 | 100.0 | 772 | AAT17259 | Coat prot |
| 5 | 69 | 100.0 | 773 | AAT34665 | Coat prot |
| 6 | 69 | 100.0 | 976 | AAQ10461 | Capsid pr |

| 7 | 69 | 100.0 | 1007 | 2 | AAQ10462 | AAQ10462 Capsid pr |
|----|----|--|--------|----|-------------|--------------------------------|
| 8 | 69 | 100.0 <th>1007</th> <th>2</th> <th>AAQ67395</th> <th>AAQ67395 Cauliflow</th> | 1007 | 2 | AAQ67395 | AAQ67395 Cauliflow |
| 9 | 69 | 100.0 <th>1066</th> <th>2</th> <th>AAT99545</th> <th>AAT99545 Cucumber</th> | 1066 | 2 | AAT99545 | AAT99545 Cucumber |
| 10 | 69 | 100.0 <th>1067</th> <th>2</th> <th>AAZ07505</th> <th>AAZ07505 Cucumber</th> | 1067 | 2 | AAZ07505 | AAZ07505 Cucumber |
| 11 | 69 | 100.0 <th>1379</th> <th>1</th> <th>AAAB1111</th> <th>AAAB1111 Sequence</th> | 1379 | 1 | AAAB1111 | AAAB1111 Sequence |
| 12 | 69 | 100.0 <th>1636</th> <th>2</th> <th>AAQ76107</th> <th>AAQ76107 Cucumber</th> | 1636 | 2 | AAQ76107 | AAQ76107 Cucumber |
| 13 | 69 | 100.0 <th>1860</th> <th>2</th> <th>AAQ76106</th> <th>AAQ76106 Cucumber</th> | 1860 | 2 | AAQ76106 | AAQ76106 Cucumber |
| 14 | 69 | 100.0 <th>2173</th> <th>2</th> <th>AAQ76108</th> <th>AAQ76108 Cucumber</th> | 2173 | 2 | AAQ76108 | AAQ76108 Cucumber |
| 15 | 64 | 92.8 <th>1423</th> <th>2</th> <th>AAQ03641</th> <th>AAQ03641 Cucumber</th> | 1423 | 2 | AAQ03641 | AAQ03641 Cucumber |
| 16 | 64 | 92.8 <th>1423</th> <th>1</th> <th>AAAB90249</th> <th>AAAB90249 Cucumber</th> | 1423 | 1 | AAAB90249 | AAAB90249 Cucumber |
| 17 | 64 | 92.8 <th>1426</th> <th>2</th> <th>AAT72272</th> <th>AAT72272 Cucumber</th> | 1426 | 2 | AAT72272 | AAT72272 Cucumber |
| 18 | 61 | 88.4 <th>894</th> <th>3</th> <th>ABLS8209</th> <th>ABLS8209 Agrobacte</th> | 894 | 3 | ABLS8209 | ABLS8209 Agrobacte |
| 19 | 45 | 65.2 <th>399</th> <th>10</th> <th>ABZ37724</th> <th>ABZ37724 N. gonorr</th> | 399 | 10 | ABZ37724 | ABZ37724 N. gonorr |
| 20 | 45 | 65.2 <th>399</th> <th>10</th> <th>ABZ41931</th> <th>ABZ41931 N. gonorr</th> | 399 | 10 | ABZ41931 | ABZ41931 N. gonorr |
| 21 | 44 | 63.8 <th>1317</th> <th>12</th> <th>ADQ61972</th> <th>ADQ61972 Transcript</th> | 1317 | 12 | ADQ61972 | ADQ61972 Transcript |
| 22 | 44 | 63.8 <th>1603</th> <th>8</th> <th>ACA38515</th> <th>ACA38515 Prokaryot</th> | 1603 | 8 | ACA38515 | ACA38515 Prokaryot |
| 23 | 44 | 63.8 <th>2208</th> <th>11</th> <th>ABD15071</th> <th>ABD15071 Pseudomon</th> | 2208 | 11 | ABD15071 | ABD15071 Pseudomon |
| 24 | 44 | 63.8 <th>2361</th> <th>11</th> <th>ABD15266</th> <th>ABD15266 Pseudomon</th> | 2361 | 11 | ABD15266 | ABD15266 Pseudomon |
| 25 | 44 | 63.8 <th>2625</th> <th>8</th> <th>ACA40580</th> <th>ACA40580 Prokaryot</th> | 2625 | 8 | ACA40580 | ACA40580 Prokaryot |
| 26 | 44 | 63.8 <th>2862</th> <th>11</th> <th>ABD14864</th> <th>ABD14864 Pseudomon</th> | 2862 | 11 | ABD14864 | ABD14864 Pseudomon |
| 27 | 44 | 63.8 <th>110000</th> <th>4</th> <th>AAI99682_22</th> <th>AAI99682_22 Continuation (23 o</th> | 110000 | 4 | AAI99682_22 | AAI99682_22 Continuation (23 o |
| 28 | 44 | 63.8 <th>110000</th> <th>4</th> <th>AAI99682_23</th> <th>AAI99682_23 Continuation (24 o</th> | 110000 | 4 | AAI99682_23 | AAI99682_23 Continuation (24 o |
| 29 | 44 | 63.8 <th>110000</th> <th>4</th> <th>AAI99683_23</th> <th>AAI99683_23 Continuation (24 o</th> | 110000 | 4 | AAI99683_23 | AAI99683_23 Continuation (24 o |
| 30 | 43 | 62.3 <th>401</th> <th>5</th> <th>AAAF6292</th> <th>AAAF6292 Novel hum</th> | 401 | 5 | AAAF6292 | AAAF6292 Novel hum |
| 31 | 43 | 62.3 <th>2000</th> <th>8</th> <th>ADA72454</th> <th>ADA72454 Rice gene</th> | 2000 | 8 | ADA72454 | ADA72454 Rice gene |
| 32 | 43 | 62.3 <th>2000</th> <th>8</th> <th>ADA72516</th> <th>ADA72516 Rice gene</th> | 2000 | 8 | ADA72516 | ADA72516 Rice gene |
| 33 | 43 | 62.3 <th>125439</th> <th>6</th> <th>ABQ88177</th> <th>ABQ88177 Human ost</th> | 125439 | 6 | ABQ88177 | ABQ88177 Human ost |
| 34 | 42 | 60.9 <th>358</th> <th>12</th> <th>ADP99136</th> <th>ADP99136 Maize cat</th> | 358 | 12 | ADP99136 | ADP99136 Maize cat |
| 35 | 42 | 60.9 <th>656</th> <th>3</th> <th>AAC50398</th> <th>AAC50398 Arabidops</th> | 656 | 3 | AAC50398 | AAC50398 Arabidops |
| 36 | 42 | 60.9 <th>657</th> <th>2</th> <th>AAQ41742</th> <th>AAQ41742 Cucumber</th> | 657 | 2 | AAQ41742 | AAQ41742 Cucumber |
| 37 | 42 | 60.9 <th>657</th> <th>2</th> <th>AAQ80683</th> <th>AAQ80683 CMV-SA co</th> | 657 | 2 | AAQ80683 | AAQ80683 CMV-SA co |
| 38 | 42 | 60.9 <th>657</th> <th>3</th> <th>AAC34260</th> <th>AAC34260 Arabidops</th> | 657 | 3 | AAC34260 | AAC34260 Arabidops |
| 39 | 42 | 60.9 <th>979</th> <th>11</th> <th>AAH92121</th> <th>AAH92121 Human inf</th> | 979 | 11 | AAH92121 | AAH92121 Human inf |
| 40 | 42 | 60.9 <th>980</th> <th>10</th> <th>ABD17977</th> <th>ABD17977 Human ade</th> | 980 | 10 | ABD17977 | ABD17977 Human ade |
| 41 | 42 | 60.9 <th>980</th> <th>10</th> <th>ABZ97241</th> <th>ABZ97241 Human ade</th> | 980 | 10 | ABZ97241 | ABZ97241 Human ade |
| 42 | 42 | 60.9 <th>981</th> <th>2</th> <th>AAQ48414</th> <th>AAQ48414 Human A1</th> | 981 | 2 | AAQ48414 | AAQ48414 Human A1 |
| 43 | 42 | 60.9 <th>981</th> <th>2</th> <th>AAT07648</th> <th>AAT07648 Human ade</th> | 981 | 2 | AAT07648 | AAT07648 Human ade |
| 44 | 42 | 60.9 <th>981</th> <th>2</th> <th>AAT29929</th> <th>AAT29929 Human ven</th> | 981 | 2 | AAT29929 | AAT29929 Human ven |
| 45 | 42 | 60.9 <th>981</th> <th>2</th> <th>AAT00644</th> <th>AAT00644 Human A1</th> | 981 | 2 | AAT00644 | AAT00644 Human A1 |

RESULT 1
AAA30858
ID AAA30858 standard; DNA, 53 BP.
AC AAA30858;
XX
DT 19-SEP-2000 (first entry)
XX
DE Ubiquitin monomer C-terminal fragment coding sequence.
XX
KW Ubiquitin monomer; protein production; plant cell; ubiquitin promoter;
KW ds.
OS Nicotiana tabacum.
XX
FH Key Location/Qualifiers
FT CDS 6..47
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FT /product= "Ubiquitin_monomer_fragment"
FT /partial
XX
XX MO200036129-A1.
XX
XX 22-JUN-2000.
XX
XX 11-DEC-1998; 98WO-SG000103.
XX
XX 11-DEC-1998; 98WO-SG000103.
XX
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
PA

| | |
|----|---|
| XX | |
| PI | Fang R, Wu J, Chen X; |
| XX | |
| DR | WPI, 2000-431604/37. |
| DR | P-PSDB; AAY90255. |
| XX | |
| PT | Production of desired protein in plants or plant cells by linking a |
| PT | ubiquitin monomer coding sequence upstream of the gene encoding the |
| XX | desired protein. |
| PS | |
| PS | Claim 8; Page 18; 42pp; English. |
| XX | |
| CC | This sequence encodes the C-terminal fragment of a ubiquitin monomer. The |
| CC | invention relates to a method for enhancing production of a desired |
| CC | protein in a plant or plant cell by inserting a nucleic acid (NA) |
| CC | encoding a ubiquitin monomer upstream of a NA encoding the desired |
| CC | protein, where the fusion construct encodes a fusion protein and |
| CC | expression is not controlled by the ubiquitin promoter. The invention |
| CC | also relates to a NA acid vector a NA vector able to transform a plant |
| CC | cell, that comprises NA encoding a fusion protein having a ubiquitin |
| CC | monomer linked to a protein of interest and further, where expression of |
| CC | the fusion construct is not under control of a ubiquitin promoter. The |
| CC | construct allows enhanced production of the desired protein in plants or |
| XX | plant cells |
| XX | |
| XX | Sequence 53 BP; 15 A; 14 C; 13 G; 11 T; 0 U; 0 Other; |

| | |
|------------------------|----------|
| Alignment Scores: | |
| Pred. No.: | 0.000262 |
| Score: | 69.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 100.00% |
| BB: | 3 |
| Length: | 53 |
| Matches: | 14 |
| Conservative: | 0 |
| Mismatches: | 0 |
| Indels: | 0 |
| Gaps: | 0 |

US-09-857-841-4 (1-14) X AAA30858 (1-53)

QY 1 MetAspPlySerGlnSerThrSerAlaGlyArgAsnArgArg 14
| | | | |
Db 6 ATGGCAAAATCTGAATCAACCAAGTGTGGTCTTAACCGTGCA 47

RESULT 2
AAT34666
ID AAT34666 standard; DNA; 771 BP.

AC AAT34666;

| | | |
|----|-------------|---------------|
| DT | 16-OCT-2003 | (revised) |
| DT | 02-DEC-1996 | (first entry) |

DE Coat protein of the V34 strain of cucumber mosaic virus.

Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35; resistance; BB.

OS Cucumber mosaic virus; strain V34.

| | Key | Location/Qualifiers |
|----|-----|---------------------|
| FH | | 3. .659 |
| FT | CDS | /*tag= a |
| FT | | |

PN WO9621018-A1

PD 11-JUL-1996

PF 07-JUN-1995; 95WO-US007234

PR 30-DEC-1994; 94US-00367789
XY

PA (ASGR-) ASGROW SEED CO.

PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
vv

...

DR WPI: 1996-333993/33.
DR P-PSDB; AAR980895.
XX
XX New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
XX
XX Claim 24; Fig 3; 80pp; English.

Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber mosaic virus (CMV) were isolated. The CMV CP genes were isolated from infected plant tissue by PCR amplification of cDNA using primers based on known CP sequences. The genes may be used for producing plants such as squash, cucumbers, peppers and tomatoes which are resistant to CMV infection. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 771 BP; 176 A; 199 C; 183 G; 213 T; 0 U; 0 Other;

| | |
|------------------------|---------|
| Alignment Scores: | |
| Pred. No.: | 0.00572 |
| Score: | 69.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 100.00% |
| DB: | 2 |
| Length: | 771 |
| Matches: | 14 |
| Conservative: | 0 |
| Mismatches: | 0 |
| Indels: | 0 |
| Gaps: | 0 |

US-09-857-841-4 (1-14) X AAT34666 (1-771

| | |
|----|---|
| Qy | 1 MetAspIyVSerCIuseRThSerAlAGLyArgenAmnArg 14 |
| | |
| Db | 3 ATGGACAAATCTGATCAACCAGTGTCTGCATACCGTCGA 44 |

RESULT 3
AAT34664
ID AAT34664 standard; DNA; 772 BP.

AC AAT34664 ;
yy

| | | |
|----|-------------|---------------|
| DT | 16-OCT-2003 | (revised) |
| DT | 02-DEC-1996 | (first entry) |

DE Coat protein of the V27 strain of cucumber mosaic virus.

KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35,
KM resistance; 88.

OS Cucumber mosaic virus; strain V27

| | Location/Qualifiers |
|-----|---------------------|
| Key | 3. .659 |
| FT | /*tag= a |
| FT | |

PN WO9621018-A1

PD 11-JUL-1996

PK 07-JUN-1995; 95MC-US007234 -
XX

XX 30-DEC-1994; 3405-0038/105-

[illegible][illegible]

DR P-PSDB; AAR98893.

PT New isolated cucumber mosaic virus coat protein DNA - used to produce plants of the family Cucurbitaceae or Solanaceae which are

PT resistant to infection

Claim 2; Fig 1; 80pp; English.

yy

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber mosaic virus (CMV) were isolated. The CMV CP genes were isolated from infected plant tissue by PCR amplification of cDNA using primers based on known CP sequences. The genes may be used for producing plants such as quash, cucumber, peppers and tomatoes which are resistant to CMV infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 772 BP; 177 A; 202 C; 182 G; 211 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | Length: | 772 |
|------------------------|---------|-----------------|
| Score: | 69.00 | Matches: 14 |
| Percent Similarity: | 100.00% | Conservative: 0 |
| Best Local Similarity: | 100.00% | Mismatches: 0 |
| Query Match: | 100.00% | Indels: 0 |
| DB: | 2 | Gaps: 0 |

US-09-857-841-4 (1-14) x AAT34664 (1-772)

QY 1 MetAspIySergIuSerThSerAlaGlyArgAsnArgArg 14
 |||||
 Db 3 ATGACAAATCTGAATCAACGAGTGTGCTGAACCGTCGG 44

RESULT 4

AAT17259
 ID AAT17259 standard; DNA; 772 BP.

XX AAT17259;

DT 16-OCT-2003 (revised)
 DT 02-DEC-1996 (first entry)

XX Coat protein of the A35 strain of cucumber mosaic virus.

XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
 KM resistance; ss.

XX Cucumber mosaic virus; strain A35.

XX Key Location/Qualifiers

FT CDS 3..659
 /*tag= a

XX MO9621018-A1.

XX 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

XX WPI; 1996-333993/33.

XX P-PSDB; AAR93803.

XX New isolated cucumber mosaic virus coat protein DNA - used to produce plants, partic. of the family Cucurbitaceae or Solanaceae, which are resistant to infection.

XX Disclousure; Fig 8; 80pp; English.

XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber mosaic virus (CMV) were isolated. The CMV CP genes were isolated from infected plant tissue by PCR amplification of cDNA using primers based on known CP sequences. The genes may be used for producing plants such as quash, cucumber, peppers and tomatoes which are resistant to CMV infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 772 BP; 175 A; 201 C; 185 G; 211 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | Length: | 772 |
|------------------------|---------|-----------------|
| Score: | 69.00 | Matches: 14 |
| Percent Similarity: | 100.00% | Conservative: 0 |
| Best Local Similarity: | 100.00% | Mismatches: 0 |
| Query Match: | 100.00% | Indels: 0 |
| DB: | 2 | Gaps: 0 |

US-09-857-841-4 (1-14) x AAT17259 (1-772)

QY 1 MetAspIySergIuSerThSerAlaGlyArgAsnArgArg 14
 |||||
 Db 3 ATGACAAATCTGAATCAACGAGTGTGCTGAACCGTCGG 44

RESULT 5

AAT34665
 ID AAT34665 standard; DNA; 773 BP.

XX AAT34665;

DT 16-OCT-2003 (revised)
 DT 02-DEC-1996 (first entry)

XX Coat protein of the V33 strain of cucumber mosaic virus.

XX Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
 KM resistance; ss.

XX Cucumber mosaic virus; strain V33.

XX Key Location/Qualifiers

FT CDS 3..659
 /*tag= a

XX MO9621018-A1.

XX 11-JUL-1996.

XX 07-JUN-1995; 95WO-US007234.

XX 30-DEC-1994; 94US-00367789.

XX (ASGR-) ASGROW SEED CO.

XX Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

XX WPI; 1996-333993/33.

XX P-PSDB; AAR98894.

XX New isolated cucumber mosaic virus coat protein DNA - used to produce plants, partic. of the family Cucurbitaceae or Solanaceae, which are resistant to infection.

XX Claim 13; Fig 2; 80pp; English.

XX Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber mosaic virus (CMV) were isolated. The CMV CP genes were isolated from infected plant tissue by PCR amplification of cDNA using primers based on known CP sequences. The genes may be used for producing plants such as quash, cucumber, peppers and tomatoes which are resistant to CMV infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 773 BP; 175 A; 200 C; 185 G; 213 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | Length: | 773 |
|------------------------|---------|-----------------|
| Score: | 69.00 | Matches: 14 |
| Percent Similarity: | 100.00% | Conservative: 0 |
| Best Local Similarity: | 100.00% | Mismatches: 0 |
| Query Match: | 100.00% | Indels: 0 |
| DB: | 2 | Gaps: 0 |

US-09-857-841-4 (1-14) x AAT34665 (1-773)

OY 1 MetAspLySeRgIuSeRThSeRAlaGlyARgAenARgArg 14
 Db 3 ATGGACAAATCTGAATCAACCAAGTCTGTCTGTAAACCTCGA 44

RESULT 6
 ID AAQ10461 standard; cDNA; 976 BP.

XX AAQ10461;

XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 16-APR-1991 (first entry)

XX Capsid protein gene of Cucumber Mosaic Virus strain FNY.

XX CMV; resistance; capsid protein; Cucumis melo; ss.

XX Cucumber mosaic virus.

XX Key Location/Qualifiers

FT CDS 75..731
 FT /*tag= a
 FT /product= "CMV strain FNY capsid protein"

XX EP412912-A.

XX 13-FEB-1991.

XX 09-AUG-1990; 90EP-00402282.

XX 11-AUG-1989; 89FR-00010848.

XX (BIOC-) BIOCEM SA.

XX Deboth M, Bentahar S, Noel M, Perret J;

XX WPI; 1991-046027/07.

XX P-PSDB; AARI0652.

XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
 PT culture on specific medium for new transformed plants etc., esp.
 PT resistant to cucumber mosaic virus.

XX Claim 15; Page 17; 44pp; French.

XX The gene was isolated from a plasmid (pUC18) containing DNA complementary
 CC to RNA 3 of the virulent strain FNY, isolated in New York on infected
 CC melons. The sequence includes a leader sequence, coding region and 3' non
 CC coding region. The leader sequence is the same length as that of the
 CC Japanese Y strain of CMV. Transgenic melon plantlets containing the
 CC sequence introduced via an Agrobacterium tumefaciens intermediate are
 CC cultured as shoots in special media. The transformed melon plants are
 CC resistant to CMV. See also AAQ10462. (Updated on 25-MAR-2003 to correct
 CC PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
 CC AUG-2003 to correct OS field.)

XX SQ Sequence 976 BP; 224 A; 249 C; 230 G; 273 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 0.00751 Length: 976
 XX Score: 69.00 Matches: 14
 XX Percent Similarity: 100.00% Conservative: 0
 XX Best Local Similarity: 100.00% Mismatches: 0
 XX Query Match: 100.00% Indels: 0
 XX DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ10461 (1-976)

OY 1 MetAspLySeRgIuSeRThSeRAlaGlyARgAenARgArg 14
 Db 75 ATGGACAAATCTGAATCAACCAAGTCTGTCTGTAAACCTCGA 116

RESULT 7
 ID AAQ10462 standard; DNA; 1007 BP.

XX AAQ10462;

XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 16-APR-1991 (first entry)

XX Capsid protein gene of Cucumber Mosaic Virus strain 117F.

XX CMV; resistance; capsid protein; Cucumis melo; ss.

XX Cucumber mosaic virus.

XX Key Location/Qualifiers

FT CDS 54..710
 FT /*tag= a
 FT /product= "CMV strain 117F capsid protein"

XX EP412912-A.

XX 13-FEB-1991.

XX 09-AUG-1990; 90EP-00402282.

XX 11-AUG-1989; 89FR-00010848.

XX (BIOC-) BIOCEM SA.

XX Deboth M, Bentahar S, Noel M, Perret J;

XX WPI; 1991-046027/07.

XX P-PSDB; AARI0653.

XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
 PT culture on specific medium for new transformed plants etc., esp.
 PT resistant to cucumber mosaic virus.

XX Claim 16; Page 19; 44pp; French.

XX The gene was isolated from the virulent French strain 117F of CMV. Tomato
 CC plantlets at the 2-leaf stage were infected with CMV strain 117F. 15 days
 CC post-infection, the virus was purified from the infected leaves and cDNA
 CC was synthesised from RNAs 1, 2, 3 and 4. After purification and selection
 CC by standard techniques, cDNA complementary to RNA 4 was found to encode
 CC the capsid protein. It was recombined into "Blue scribe" plasmids and
 CC sequenced. Transgenic melon plantlets containing the sequence introduced
 CC via an Agrobacterium tumefaciens intermediate are cultured as shoots in
 CC special media. The transformed melon plants are resistant to CMV. See
 CC also AAQ10461. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 CC 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
 CC field.)

XX SQ Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 0.00778 Length: 1007
 XX Score: 69.00 Matches: 14
 XX Percent Similarity: 100.00% Conservative: 0
 XX Best Local Similarity: 100.00% Mismatches: 0
 XX Query Match: 100.00% Indels: 0
 XX DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ10462 (1-1007)

OY 1 MetAspLySeRgIuSeRThSeRAlaGlyARgAenARgArg 14
 Db 54 ATGGACAAATCTGAATCAACCAAGTCTGTCTGTAAACCTCGA 95

RESULT 8

AA067395
ID AA067395 standard; DNA; 1007 BP.
XX
XX AA067395;
XX
XX 25-MAR-2003 (revised)
DT 12-APR-1995 (first entry)
XX
XX Cauliflower mosaic virus capsid protein coding sequence.
DE
XX Cauliflower mosaic virus; CMV; capsid protein; coat protein;
KM polynibozyme; inactivate; inactivation; resistance; crop protection; ss.
XX
XX Cauliflower mosaic virus.
XX
XX Key Location/Qualifiers
FT CDS 54..710
FT /*tag= a
FT /product= "Capsid protein."
XX
XX FR2701960-A1.
XX
XX 02-SEP-1994.
XX
XX 26-FEB-1993; 93FR-00002269.
XX
XX 26-FEB-1993; 93FR-00002269.
XX
XX (GENE-) GENE SHEARS PTY LTD.
XX
XX Lenee P, Perez P, Gruber V, Baudot G, Ollivo C;
PI
XX
XX WPI: 1994-281767/35.
DR P-PSDB; AAR57968.
XX
XX New polynibozyme contg. several catalytic regions in complementary
PT sequence - can inactivate gene for viral capsid protein, esp. for prepn.
PT of new virus resistant transgenic plants, also DNA sequence encoding it.
XX
XX Disclosure; Fig 2; 67pp; French.
XX
XX The RNA encoding the capsid protein of cauliflower mosaic virus can be
CC targeted by a nucleic acid sequence called a "polynibozyme". The
CC polynibozyme has endonuclease activity and is able to inactivate the
CC gene encoding the viral capsid protein. The polynibozyme comprises
CC several catalytic regions derived from ribozymes and confers complete
CC resistance to virus. See AA067391-94. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
XX Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0.00778 Length: 1007
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-857-841-4 (1-14) x AA067395 (1-1007)
QY 1 MetAspIysSerGluSerThrSerAlaGlyArgAsnArg 14
DB 54 ATGACCAATCTGAATCAACCAAGTCTGTCGTAAACCTGCA 95
RESULT 9
AAT99545/c
ID AAT99545 standard; CDNA; 1066 BP.
XX
XX AAT99545;
XX
XX 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)

XX
XX Cucurbit mosaic virus RNA-3 CDNA fragment.
DE
XX Transgenic plant; virus resistance; disease resistance; RNA virus; CMV;
KM coat protein; antisense gene; ss.
XX
XX Cucurbit mosaic virus.
XX
XX Key Location/Qualifiers
FT 3'UTR 1..299
FT /*tag= a
FT CDS 300..958
FT /*tag= b
FT /product= "coat protein"
FT sig_peptide 956..1029
FT /*tag= c
FT /note= "coat protein leader sequence"
FT 1030..1066
FT /*tag= d
FT /note= "F sequence of sub-genomic promoter"
XX
XX EP806481-A2.
XX
XX 12-NOV-1997.
XX
XX 07-MAY-1997; 97BP-00201379.
XX
XX 09-MAY-1996; 96IT-M1000927.
XX
XX (META-) METAPONTUM AGROBIOS SCRL.
XX
XX Cellini F, Grieco PD;
PI
XX
XX WPI: 1997-538620/50.
XX
XX Preparing transgenic plants resistant to RNA virus infection - using
PT anti-sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
XX Claim 3; Page 10; 18pp; English.
XX
XX This CDNA clone of cucumber mosaic virus (CMV) RNA-3 includes domain F of
CC the subgenomic promoter of viral RNA, the coat protein gene, its leader
CC sequence, and the RNA-like 3'-terminal region of RNA-3. It was prepared
CC by amplifying a fragment of CMV CDNA-3 from clone PCR-CMV1RNA3 by PCR
CC (see also AAT99548-49). The gene construct is introduced into a vector
CC containing a promoter active in plant cells in antisense orientation
CC relative to the promoter. A claimed recombinant vector comprises the
CC plant promoter, the antisense gene construct and a terminator which is
CC functional in the plant. In addition to CMV, viral RNA may also be used
CC from tobacco mosaic virus and potato virus. Claimed transgenic plants
CC have the antisense gene construct integrated into their genomes. They are
CC resistant to viral infection. In particular, they are resistant to CMV.
CC Within the antisense gene construct, the interfering activity of the
CC antisense F domain of the sub-genomic promoter, associated with the
CC antisense activity performed by the coat protein gene, allows production
CC of plants having 100% resistance to CMV. (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
XX Sequence 1066 BP; 299 A; 251 C; 273 G; 243 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0.00831 Length: 1066
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-857-841-4 (1-14) x AAT99545 (1-1066)
QY 1 MetAspIysSerGluSerThrSerAlaGlyArgAsnArg 14

Db 956 ATGACAAATCTGAATCAACGAGTGGTGGTAAACCGTCGA 915
RESULT 10
ID AA207505 standard; cDNA, 1067 BP.
XX AA207505;
AC
XX 26-NOV-1999 (first entry)
DT
XX Cucurbit mosaic virus (CMV) RNA-3 gene cDNA clone fragment.
DE
XX Transgenic plant; RNA virus; antisense construct; cucumber mosaic virus;
KM CMV; promoter; coat protein gene; infection; RNA-3; ss.
XX
XX Cucurbit mosaic virus.
OS
XX US5959181-A.
PN
XX 28-SEP-1999.
PD
XX 09-MAY-1997; 97US-00854170.
PF
XX 09-MAY-1996; 96IT-MI000927.
PR
XX (META-) METAPONTUM AGROBIOS SCRL.
PA
XX Cellini F, Grieco PD;
PI
XX WPI; 1997-538620/50.
DR
XX
XX Preparing transgenic plants resistant to RNA virus infection - using
PT anti-sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
XX Claim 2; Fig 1; 15pp; English.
PS
XX The invention relates to preparing transgenic plants resistant to RNA
CC virus induced infections that comprises integrating an antisense gene
CC construct into the plant genome. The construct comprises: (a) an F domain
CC of a subgenomic promoter of cucumber mosaic virus (CMV); (b) downstream
CC from the subgenomic promoter, a leader sequence of a coat protein gene of
CC CMV; (c) downstream from the leader sequence, a gene encoding a CMV coat
CC protein; and (d) downstream from the gene, a 3'-terminal region of a CMV
CC coat protein gene. The method is useful for producing plants which are
CC resistant to infection by RNA based viruses. The gene construct gives
CC higher levels of resistance compared to antisense constructs which are
CC capable of complementing with different domains of genomic RNA of CMV.
CC The present sequence represents the fragment of cDNA clone of RNA-3 of
CC CMV. This forms the antisense construct of the invention
XX
XX Sequence 1067 BP; 297 A; 250 C; 276 G; 244 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0.00832 Length: 1067
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-857-841-4 (1-14) x AA207505 (1-1067)
OY 1 MetaphySergUserThSeraIaGIvARgAsnARg 14
ID AA207505 standard; cDNA, 1067 BP.
XX
XX 956 ATGACAAATCTGAATCAACGAGTGGTGGTAAACCGTCGA 915
RESULT 11
ID AA207505 standard; DNA, 1379 BP.
XX
XX AA207505;
AC
XX
XX

DT 25-MAR-2003 (revised)
DT 12-NOV-1990 (first entry)
XX
XX Sequence contg. CMV strain Y coat protein gene.
DE
XX Cucurbit mosaic virus; plant viral resistance; ss.
KM
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FT CDS 418..1074
FT /tag= a
FT /label= cucumber mosaic virus-Y coat protein.
EP279433-A.
XX
XX 24-AUG-1988.
PD
XX 18-FEB-1988; 88EP-00102322.
PF
XX 20-FEB-1987; 87JP-00038288.
PR 25-FEB-1987; 87JP-00043443.
PR 18-FEB-1988; 88JP-00035809.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
PA
XX Furusawa I, Onda H, Komiya T;
PI
XX WPI; 1988-236708/34.
DR P-PSDB; AAP80509.
XX
XX DNA coding for the coat protein of cucumber mosaic virus strain Y - used
PT for producing plants resistant to cucumber mosaic virus infection.
PT
XX
XX Disclosure; Page 7; 20pp; English.
PS
XX This DNA is produced on screening of a plasmid library and is used to
CC transform plant cells which subsequently produce the coat prot- ein of
CC cucumber mosaic virus (CMV) strain Y. This protein is not synthesised in
CC natural plant cells. The resistance to CMV infect- ion, provided by the
CC DNA, is shown in plant cells and redifferent- iated plant bodies. See
CC also AA207505. (Updated on 25-MAR-2003 to correct PR field.) (Updated on
CC 25-MAR-2003 to correct PA field.)
XX
XX Sequence 1379 BP; 306 A; 342 C; 333 G; 398 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0.0112 Length: 1379
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-857-841-4 (1-14) x AA207505 (1-1379)
OY 1 MetaphySergUserThSeraIaGIvARgAsnARg 14
ID AA207505 standard; DNA, 1379 BP.
XX
XX AA207505;
AC
XX 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
DT
XX Cucurbit mosaic virus RNA-3 chimera encoding RNase TI.
DE
XX Cucurbit mosaic virus; tomato mosaic virus; minus-strand RNA;
KM virus resistance; disease resistance; transgenic plant; cross protection;
KM

| | |
|-----------|--|
| XX | Cucumber mosaic virus. |
| OS | |
| XX | |
| FH | Key |
| FT | Location/Qualifiers |
| FT | 123..600 |
| FT | /tag= a |
| FT | /product= "TomV coat protein" |
| FT | 895..1550 |
| FT | /tag= b |
| FT | /product= "CMV coat protein" |
| FN | |
| XX | |
| XX | MO9429464-A1. |
| XX | |
| PD | 22-DEC-1994. |
| XX | |
| PF | 03-JUN-1994; |
| XX | 94MO-BP001817. |
| PR | 04-JUN-1993; |
| XX | 93GB-00011593. |
| PA | (SANO) SANDOZ LTD. |
| PA | (SANO) SANDOZ PATENT GMBH. |
| PA | (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH. |
| PI | De Haan PT; |
| XX | |
| DR | WPI; 1995-036490/05. |
| DR | P-PADB; AAR67752, AAR67753. |
| PT | DNA constructs for imparting pathogen, esp. virus, resistance to plants - |
| PT | encodes RNA that interacts with viral RNA polymerase to generate an |
| PT | eliciting agent. |
| XX | |
| PS | Claim 3; Page 27-28; 50pp; English. |
| XX | |
| CC | A chimeric cucumber mosaic virus RNA-3 (given in AAQ76106) codes for the |
| CC | cucurbit protein (CP) of tomato mosaic virus (AAR67752) as well as its own CP |
| CC | (AAR67753). The construct elicits minus-sense RNA that interacts with the |
| CC | RNA-dependent RNA-polymerase of an invading virus, thus conferring virus |
| CC | resistance on a host plant, e.g. tobacco, tomato. (Updated on 25-MAR-2005 |
| CC | to correct PN field.) |
| XX | |
| SQ | Sequence 1860 BP; 448 A; 429 C; 431 G; 552 T; 0 U; 0 Other; |
| | |
| | Alignment Scores: |
| | Pred. No.: |
| | Score: 0.0158 Length: 1860 |
| | Percent Similarity: 69.00 Matches: 14 |
| | Best Local Similarity: 100.00% Conservative: 0 |
| | Mismatches: 0 |
| | Query Match: 100.00% Indels: 0 |
| | Gaps: 0 |
| | DB: 2 |
| | |
| Oy | US-09-857-841-4 (1-14) x AAQ76106 (1-1860) |
| Db | 1 MetaspIysSerGIuserThierlaGlytArganaARGatg 14 897 ATGCACAAATCGAATCAACAGCTGTCGTGAACCGTCA 938 |
| RESULT 14 | |
| ID | AAQ76108 standard; DNA; 2173 BP. |
| XX | |
| AC | AAQ76108; |
| XX | |
| DT | 25-MAR-2003 (revised) |
| DT | 20-JUL-1995 (first entry) |
| XX | |
| DE | Cucumber mosaic virus RNA-3 chimera encoding TomV P30. |
| XX | |
| KM | Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA; |
| KM | virus resistance; disease resistance; transgenic plant; cross protection; |
| KM | hypersensitive response; crop improvement; tomato; |
| KM | Lycopersicon esculentum; tobacco; Nicotiana tabacum; P30; elicitor; TomV/CNV; ss. |

```
XX OS Cucurbit mosaic virus.
XX
XX Key Location/Qualifiers
XX CDS 123..914
XX FT /*tag= a
XX FT /product= "TOMV P30 elicitor"
XX
XX PN MO9429464-A1.
XX
XX PD 22-DEC-1994.
XX
XX PF 03-JUN-1994; 94WO-EP001817.
XX
XX PR 04-JUN-1993; 93GB-00011593.
XX
XX PA (SANO ) SANDOZ LTD.
XX PA (SANO ) SANDOZ PATENT GMBH.
XX PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
XX PI De Haan PT;
XX
XX DR WPI: 1995-036490/05.
XX DR P-PSDB; AAR67755.
XX
XX PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
XX PT encodes RNA that interacts with viral RNA polymerase to generate an
XX PT eliciting agent.
XX
XX PS Claim 5; Page 34-35; 50pp; English.
XX
XX CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76108) has the coat
XX CC protein gene replaced by a gene encoding an elicitor, TOMV P30, having
XX CC the sequence given in AAR67755. The construct elicits a minus-gense RNA
XX CC that interacts with the RNA-dependent RNA-polymerase of an invading
XX CC virus, thus conferring virus-resistance on a host plant, e.g. tobacco,
XX CC tomato. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 2173 BP; 561 A; 438 C; 532 G; 642 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0189 Length: 2173
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ76108 (1-2173)
QY 1 MetaspIySergIuSerThrSerIaGlyArgAsnArg 14
Db 1210 ATGGACAATCTGAATCAACCAAGTCTGTGTAACCTCGA 1251

RESULT 15
AAQ03641
ID AAQ03641 standard; DNA; 657 BP.
XX
XX AC AAQ03641;
XX
XX DT 24-OCT-2003 (revised)
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 07-AUG-1990 (first entry)
XX
XX DE Cucurbit Mosaic Virus-C (CMV-C) coat protein gene.
XX
XX KM CMV-C; curcubitaceae; solanaceae; ds.
XX
XX OS Cucurbit mosaic virus; strain C.
XX
XX PN MO9002185-A.
XX
```

```
PD 08-MAR-1990.
XX
XX PF 02-AUG-1989; 89WO-US003288.
XX
XX PR 19-AUG-1988; 88US-00234404.
XX
XX PA (UPJO ) UPJOHN CO.
XX PA (CORR ) CORNELL RES FOUND INC.
XX
XX PI Quemada H, Slightom JL, Gonsalves D, Kearney C;
XX
XX DR WPI: 1990-099409/13.
XX
XX PT Coat protein gene of cucumber mosaic virus strain WL - cloned to produce
XX PT transformed plants which are resistant to CMV viral infection.
XX
XX PS Disclosure; Page ?; 18pp; English.
XX
XX CC The sequence encodes the coat protein of CMV-C. (Updated on 25-MAR-2003
XX CC to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)
XX CC (Updated on 27-AUG-2003 to correct OS field.) (Updated on 24-OCT-2003 to
XX CC standardise OS field)
XX
XX SQ Sequence 657 BP; 157 A; 176 C; 151 G; 173 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.0379 Length: 657
Score: 64.00 Matches: 13
Percent Similarity: 92.86% Conservative: 0
Best Local Similarity: 92.86% Mismatches: 1
Query Match: 92.75% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ03641 (1-657)
QY 1 MetaspIySergIuSerThrSerIaGlyArgAsnArg 14
Db 1 ATGGACAATCTGAATCAACCAAGTCTGTGTAACCATCGA 42
```

Search completed: December 5, 2004, 08:24:35
Job time : 329 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 08:17:23 ; Search time 2044 Seconds
(without alignments)
249.587 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSAQRNR 14

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Pgapop 6.0 , Pgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+g2n.model -DEV=xlh
-O=/cgn1/USPRO.epool/US09857841/runat_03122004_160551_18593/app.query.fasta_1.199
-DB=EST -QFMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=humand4.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USR=US09857841 @CGN_1_1_3437 @runat_03122004_160551_18593 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEDBPRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_g881.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| C 1 | 69 | 100.0 | 127 | 4 | BM067231 KS08001E1 |
| C 2 | 49 | 71.0 | 416 | 2 | BR023342 sm70f09.Y |
| C 3 | 49 | 71.0 | 443 | 6 | CA800884 sam26b02. |
| C 4 | 49 | 71.0 | 456 | 4 | BT468772 gal33c10. |
| C 5 | 49 | 71.0 | 544 | 4 | BT468772 gal33c10. |
| C 6 | 48 | 69.6 | 617 | 8 | AQ737846 HS_2167_A |
| C 7 | 48 | 69.6 | 956 | 9 | CC978898 ZUAG628TH |
| C 8 | 47 | 68.1 | 594 | 7 | CF568862 FAMU USDA |
| C 9 | 46 | 66.7 | 413 | 1 | AL584972 AL584972 |

| | | | | | |
|------|----|------|------|---|----------|
| 10 | 46 | 66.7 | 480 | 1 | AL836204 |
| C 11 | 46 | 66.7 | 486 | 5 | BX256743 |
| C 12 | 46 | 66.7 | 490 | 5 | BX256742 |
| C 13 | 46 | 66.7 | 645 | 6 | CD356033 |
| C 14 | 46 | 66.7 | 653 | 7 | CF577172 |
| C 15 | 46 | 66.7 | 677 | 9 | AG540710 |
| C 16 | 46 | 66.7 | 703 | 9 | BU340711 |
| C 17 | 46 | 66.7 | 709 | 9 | CE629751 |
| C 18 | 46 | 66.7 | 754 | 5 | BU109941 |
| C 19 | 46 | 66.7 | 760 | 5 | BU366212 |
| C 20 | 46 | 66.7 | 804 | 5 | BU261839 |
| C 21 | 46 | 66.7 | 813 | 5 | BU256140 |
| C 22 | 46 | 66.7 | 815 | 5 | BU227211 |
| C 23 | 46 | 66.7 | 842 | 5 | BU323014 |
| C 24 | 46 | 66.7 | 892 | 5 | BU134521 |
| C 25 | 46 | 66.7 | 1829 | 4 | EM542237 |
| C 26 | 45 | 65.2 | 363 | 8 | AQ770244 |
| C 27 | 45 | 65.2 | 399 | 2 | AM752426 |
| C 28 | 45 | 65.2 | 429 | 9 | CC860753 |
| C 29 | 45 | 65.2 | 504 | 1 | AI930097 |
| C 30 | 45 | 65.2 | 565 | 6 | CB241923 |
| C 31 | 45 | 65.2 | 675 | 7 | CF881443 |
| C 32 | 45 | 65.2 | 690 | 9 | CE056926 |
| C 33 | 45 | 65.2 | 744 | 6 | CF250879 |
| C 34 | 45 | 65.2 | 754 | 5 | BU271993 |
| C 35 | 45 | 65.2 | 791 | 8 | CC401658 |
| C 36 | 45 | 65.2 | 827 | 9 | CC692105 |
| C 37 | 45 | 65.2 | 1093 | 4 | EG404055 |
| C 38 | 44 | 63.8 | 248 | 2 | BF519533 |
| C 39 | 44 | 63.8 | 315 | 1 | AV161127 |
| C 40 | 44 | 63.8 | 400 | 8 | AZ049482 |
| C 41 | 44 | 63.8 | 404 | 2 | AM127447 |
| C 42 | 44 | 63.8 | 413 | 1 | AJ502914 |
| C 43 | 44 | 63.8 | 422 | 5 | BQ164765 |
| C 44 | 44 | 63.8 | 471 | 8 | AQ863793 |
| C 45 | 44 | 63.8 | 476 | 1 | AL369661 |

ALIGNMENTS

RESULT 1
LOCUS BM067231/C
DEFINITION KS08001E12 KS08 Capsicum annuum cDNA, mRNA sequence.
ACCESSION BM067231
VERSION BM067231.1 GI:22787366
KEYWORDS EST.
SOURCE Capsicum annuum
ORGANISM Capsicum annuum

REFERENCE
AUTHORS Lee,S., Kim,S.-Y., Chung,Y.-H., Shin,H.-J., Goh,S.-H., Pal,H.-S., Hur,C.-G. and Choi,D.
1 (bases 1 to 127)
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Capsicum.

TITLE
JOURNAL
COMMENT
Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen
Unpublished (2001)
Contact: Doil Choi
Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea
Tel: 82-42-860-4340
Fax: 82-42-860-4309
Email: doilchoi@kribb.re.kr
High quality sequence stop: 127.

FEATURES

source
1..127
/organism="Capsicum annuum"
/mol_type="mRNA"
/cultivar="Hang Keun"
/db_xref="taxon:4072"

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ORIGIN
/issue_type="anther"
/dev_stage="10 weeks after germination"
/clone_lib="KS08"
/notes="Vector: pbluescript SK(-)"

Alignment Scores:
Pred. No.: 0.00679 Length: 127
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-857-841-4 (1-14) x BM067231 (1-127)

QY 1 MetApIySergIuSerThrSerAlaGlyArgAsnArgArg 14
Db 78 ATGACAAATCTGATCAACGAGTGTGTGTAACCGTCGA 37

RESULT 2
BE023342/c BE023342 416 bp mRNA linear EST 24-JUL-2004
LOCUS em70f09.y1 Gm-cl028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl028-9282 5' similar to TR:Q13437 Q13437 DELETED IN SPLIT
HAND/SPLIT FOOT 1 ; mRNA sequence.
BE023342
VERSION BE023342.1 GI:8285783
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 416)
Shoemaker,R., Keim,P., Vodkin,L., Erpellding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,I., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Riteyer,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCam,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Other ESTs: B1971551 corresponding to Gm-r1083-4800 (3')
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: east@wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 1035 Std Error: 0.00.

FEATURES
Source
Location/Qualifiers
1..416
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Superiod"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl028-9282"
/issue_type="roots of 'Superiod' plants"
/lab_host="DHL08"
/clone_id="Gm-cl028"
/notes="Vector: pbluescript II XR; Site 1: EcoRI; Site 2:
XhoI. The mRNA was isolated from roots of Glycine max
'Superiod' plants generously donated by Dr. Gary Stacey.
The seedlings were inoculated with Bradyrhizobium
japonicus, strain USDA110 prior to harvest. StrataGene's
cDNA synthesis kit (catalog number 200401) was used to

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synthesize the cDNA. First-strand synthesis was performed
with 5-methyl dCTP, hence the ligated cDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An 'anchor'
nucleotide (V=A,C, or G) was added to the 3' end of the
primer [GAGAGAGAGAGAGAGAACTACTCTCGAG(T)18V] to anchor
the primer at the 5' end of the poly(A) tract. After
second-strand synthesis, the cDNA ends were filled in with
cloned Pfu DNA polymerase, ligated to EcoRI adapters and
subsequently phosphorylated. The XhoI site within the
first-strand synthesis primer was then restricted by
digestion with XhoI; all XhoI sites in the cDNA would be
protected by their hemimethylated status. The cDNA
constructs were size-fractionated with a 500bp cutoff,
using GibcoBRL Life Technologies' cDNA Size Fractionation
column. The column eluent was then ligated into
Stratagene's pbluescript II XR predigested vector
(pbluescript II SK(+)) that has been digested with EcoRI
and XhoI, and phosphorylated by Stratagene). Both the
white and blue colonies appear to contain recombinant
plasmids with cDNA inserts, based on size (n=25). This
library was constructed by Dr. Paul Keim and Dr. Virginia
Coryell."

ORIGIN
Alignment Scores:
Pred. No.: 92.7 Length: 416
Score: 49.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 71.01% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x BE023342 (1-416)

QY 1 MetApIySergIuSerThrSerAlaGlyArgAsnArgArg 14
Db 123 ATGACAAAGCCGATCTACCGCTGTGGAAGAAACGAAGA 82

RESULT 3
CA800884/c CA800884 443 bp mRNA linear EST 01-JUL-2004
LOCUS bat26b02.y1 Gm-cl056 Glycine soja cDNA clone SOYBEAN CLONE ID:
Gm-cl056-2379 5' similar to TR:Q9XIR8 Q9XIR8 F13011.6 PROTEIN. ;
mRNA sequence.
CA800884
VERSION CA800884.1 GI:26057970
KEYWORDS EST.
SOURCE Glycine soja
ORGANISM Glycine soja
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 443)
Shoemaker,R., Keim,P., Vodkin,L., Erpellding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,I., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Riteyer,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCam,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: east@wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD

```


FEATURES

SOURCE

57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers

1. .443

/organism="Glycine soja"
/mol_type="mRNA"
/db_xref="taxon:3848"
/clone="SOYBEAN CLONE ID: Gm-c1056-2379"
/tissue_type="whole seedling, 4 day old"
/lab_host="DH10B"
/clone_lib="Gm-c1056"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from 4 day old seedling of PI468916. The seedlings were germinated in a growth chamber using germination paper. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Alignment Scores:

Pred. No.: 98.8 Length: 443
Score: 49.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 71.01% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x CA800884 (1-443)

QY 1 MetApLySerGIuSerThrSerAlaGlyArgAsnArgArg 14
DB 112 ATGGACAAAGCCGATCTACCGCTGTGGAGAACGAAAGA 71

RESULT 4

BI468772/c

LOCUS BI468772 456 bp mRNA linear EST 08-JUL-2004
DEFINITION BAI03c10.y1 Gm-c1050 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1050-4363 5' similar to TR:Q9XIR8 Q9XIR8 F13011.6 PROTEIN.
; mRNA sequence.

ACCESSION BI468772

VERSION BI468772.1 GI:15284890

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM

Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

1 (bases 1 to 456)

REFERENCE

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Materon, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this

FEATURES

SOURCE

clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 3rd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 360.
Location/Qualifiers

1. .456

/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Clark"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1050-4363"
/tissue_type="leaf tissue at various developmental stages
of greenhouse grown plants"
/dev_stage="3 week old"
/lab_host="DH10B"
/clone_lib="Gm-c1050"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The Clark NIL was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Specht, 1995). The cDNA library was constructed from mRNA
isolated from leaf tissue at various developmental stages
of 3 week old greenhouse grown plants. Complementary DNA
was synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site and a 3'
anchor. EcoRI adapters were ligated to the blunt-ended
cDNA fragments followed by XhoI digestion. The cDNA
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
(GibcoBRL). The library was constructed in cooperation
with Dr. Paul Keim's laboratory at Northern Arizona
University."

ORIGIN

Alignment Scores:

Pred. No.: 102 Length: 456
Score: 49.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 71.01% Indels: 0
DB: 4 Gaps: 0

US-09-857-841-4 (1-14) x BI468772 (1-456)

QY 1 MetApLySerGIuSerThrSerAlaGlyArgAsnArgArg 14
DB 85 ATGGACAAAGCCGATCTACCGCTGTGGAGAACGAAAGA 44

RESULT 5

BI971551

LOCUS BI971551 544 bp mRNA linear EST 23-OCT-2001
DEFINITION GM63001321D12 Gm-r1083 Glycine max cDNA clone Gm-r1083-4800 3',
mRNA sequence.

ACCESSION BI971551

VERSION BI971551.1 GI:16345956

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM

Glycine max (soybean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

1 (bases 1 to 544)

REFERENCE

AUTHORS

Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V.,
Erpelting, J., Rapp, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H.
A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)

Other ESTs: BE023342 corresponding to Gm-c1028-9282 (5')

Contact: Vodkin, L.O., PI, A Functional Genomics Program for

Soybean (NSF 9872565)

Lewin, H. A., Director, Keck Center for Comparative and Functional

Genomics
University of Illinois

Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
 Tel: (217) 244-6147
 Fax: (217) 333-4582
 Email: l.vodkin@uiuc.edu
 This clone is available through: Incyte Genomics, 4633 World
 Parkway Circle St. Louis, Missouri 63134. Phone (800) 430-0030 or
 (314) 427-3222 FAX: (314) 427-3324. Web site:
 http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboratio
 n/index

Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'.

FEATURES

source

Location/Qualifiers

1..544
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="Gm-r1083-4800"
 /clone_1b="Gm-r1083"
 /note="The library Gm-r1083 is a sequence-driven, reracked
 set of 4,992 clones selected from cDNA libraries from
 various tissues and stages of development of soybean. It
 represents 1117 sequences from the progenitor library
 Gm-c1009 (from mature roots of 2 month old greenhouse
 grown 'Williams' soybean plants); 820 sequences from the
 progenitor library Gm-c1013 (from 2 to 3 week old whole
 plants of Williams); and 3055 sequences from library
 Gm-c1028 (from 'Superpod' plants whose seedlings were
 inoculated with *Bradyrhizobium japonicum*, courtesy of Dr.
 Gary Stracey). The 5' ESTs of the source clones from the
 different progenitor libraries was used to select
 singletons, or a representative of each contig, which were
 reracked to form library Gm-r1083. The cDNA clones of the
 reracked Gm-r1083 library were then sequenced at the 3'
 end. The contig analysis to select unique genes was
 performed by the laboratory of Ernest Reizel, Center for
 Computational Genomics and Bioinformatics, University of
 Minnesota, http://web.ahc.umn.edu/biodata/nafsioy/.
 Reracking was performed by Incyte Genomics, St. Louis,
 http://www.incyte.com, and 3' sequencing by the Keck
 Center for Comparative and Functional Genomics, University
 of Illinois, http://www.lie.uiuc.edu/bioec/keck.html.
 Note: The corresponding 5' EST from each clone in the
 Gm-r1083 library is listed in the 'OTHER EST' field. The
 detailed information on the source library for each clone
 can also be obtained by referring to the Incyte Genomics
 clone ID of the original cDNA library that is also listed
 under 'OTHER EST'."

ORIGIN

Alignment Scores:

Pred. No.: 122 Length: 544
 Score: 49.00 Matches: 9
 Percent Similarity: 78.57% Conservative: 2
 Best Local Similarity: 64.29% Mismatches: 3
 Query Match: 71.01% Indels: 0
 DB: 4 Gaps: 0

US-09-857-841-4 (1-14) x B1971551 (1-544)

Qy 1 MetaspysSergJuserThSeraIaGlyArqAmaArg 14
 Db 421 ATGACAAAGCCGATCTACCGCTGTGGAGAAACAAAGA 462

RESULT 6

LOCUS AQ737846/c 617 bp DNA linear GSS 16-JUL-1999
 DEFINITION HS-2167_A1-B08-T7C CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=2167 Col=15 Row=C, genomic survey
 sequence.

ACCESSION AQ737846
 VERSION AQ737846.1 GI:5515368
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 617)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 Sequence-tagged connectore: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 99380589
 10449764
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 2167 row: C column: 15
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 617.
 Location/Qualifiers

FEATURES

source

1..617
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=2167 Col=15 Row=C"
 /sex="male"
 /clone_1b="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelBAC11; BAC clones in
 E-Coli DH10B"

ORIGIN

Alignment Scores:

Pred. No.: 210 Length: 617
 Score: 48.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 6
 Best Local Similarity: 57.14% Mismatches: 0
 Query Match: 69.57% Indels: 0
 DB: 8 Gaps: 0

US-09-857-841-4 (1-14) x AQ737846 (1-617)

Qy 1 MetaspysSergJuserThSeraIaGlyArqAmaArg 14
 Db 596 ATAGATCAAAATGATCAAGCTCAAGCGCGCTAATGAAGG 555

RESULT 7

LOCUS CC978898/c 956 bp DNA linear GSS 18-AUG-2003
 DEFINITION ZUAG628TH ZM_3_0_4_0_XB Zee mays genomic clone ZMBBP8057F07,
 genomic survey sequence.

ACCESSION CC978898
 VERSION CC978898.1 GI:33838776
 KEYWORDS GSS.
 SOURCE Zee mays
 ORGANISM Zee mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zee.
 1 (bases 1 to 956)
 Whiteaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Reenick,A., Frazer,C.M., Budiman,M.A., Bedell,J.A., Kohlfing,T.,
 Citek,R.W., Nuneberg,A., Robbins,D. and Lakey,N.
 Consortium for Maize Genomics
 Unpublished (2002)
 Other GSSs: ZUAG628TV
 Contact: Cathy Whiteaw
 TIGR

7972 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteja@ligr.org
Seq primer: TR
Class: sheared ends
Location/Qualifiers

FEATURES
source 1..956

/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBPa005F07"
/clone_1lb="ZM 3.0 4.0 KB"
/note="Vector: pBOSK-; Site_1: HincII; 3-4 kb 'unfiltered'
genomic DNA library"

ORIGIN

Alignment Scores:

Pred. No.: 329 Length: 956
Score: 48.00 Matches: 8
Percent Similarity: 85.71% Conservative: 4
Best Local Similarity: 57.14% Mismatches: 2
Query Match: 69.57% Indels: 0
DB: 9 Gaps: 0

US-09-857-841-4 (1-14) x CC978898 (1-956)

Qy 1 MetaplyserGluSerTherSerAlaGlyArgAsnArg 14

Db 213 CTGGACAAAGACAGACAGCCGCTGGAGAAACCGCGG 172

RESULT 8 CFS68862 594 bp mRNA linear EST 23-SEP-2003

LOCUS FAMU_USDA_FP_00084 Vitis shuttleworthii L., grape Vitis

shuttleworthii cDNA 5', mRNA sequence.

ACCESSION CFS68862

VERSION CFS68862.1 GI:34994945

KEYWORDS EST.

SOURCE Vitis shuttleworthii

ORGANISM Vitis shuttleworthii

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; Vitaceae; Vitis.

1 (bases 1 to 594)

Hunter, W.B., Dang, P.M., Chaparro, J.X., Lu, J. and Leong, S.

Genes expressed in Vitis shuttleworthii L

Unpublished (2004)

Contact: Jiang Lu, FAMU, Wayne Hunter, USDA, ARS

Florida A&M University, Tallahassee, FL 32317, USA

Tel: (850) 412-7393

Fax: (850) 561-2617, (772) 462-5898

Email: jiang.lu@famr.edu,

Seq primer: T3 Primer.

Location/Qualifiers

1..594

/organism="Vitis shuttleworthii"

/mol_type="mRNA"

/db_xref="taxon:246827"

/set="Mixed population"

/tissue_type="Entire tendril, leaves, bud, flowers"

/dev_stage="At blooming"

/lab_host="XLI-Blue"

/clone_1lb="Vitis shuttleworthii L., grape"

/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:

XhoI; A high quality EST with at least 10 contiguous

bases at trace runner score of 20 or better. Construction

by PW Dang, USDA, ARS, U.S. Horticultural Research Lab,

FL, Pierce, FL, USA."

ORIGIN

Alignment Scores:
Pred. No.: 306 Length: 594
Score: 47.00 Matches: 9
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 81.82% Mismatches: 0
Query Match: 68.12% Indels: 0
DB: 7 Gaps: 0

US-09-857-841-4 (1-14) x CFS68862 (1-594)

Qy 4 SerGluSerTherSerAlaGlyArgAsnArg 14

Db 73 ACAGAGCAACATCTGACGGAGAAATCGGAGA 105

RESULT 9

AL584972/c 413 bp mRNA linear EST 28-FEB-2001

LOCUS AL584972 Stratiagene Chick Embryo Lambda cDNA Library (* 937405)

DEFINITION Gallus gallus cDNA clone ROS016G12, mRNA sequence.

ACCESSION AL584972 GI:13163705

VERSION AL584972.1 GI:13163705

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 413)

Murray, F.

Stratiagene Chick Embryo Lambda cDNA Library

Unpublished (2001)

Contact: Frazer Murray

Dept. Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UK

Tel: +44 (0)131 527 4200

Fax: +44 (0)131 440 0434

Email: frazer.murray@berc.ac.uk

Seq primer: T3.

Location/Qualifiers

1..413

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="ROS016G12"

/tissue_type="Embryo"

/dev_stage="5 days old"

/lab_host="SOLR cells (kanamycin resistant)"

/clone_1lb="Stratiagene Chick Embryo Lambda cDNA Library (*

937405)"

/note="Vector: pBluescript SK, Site_1: EcoRI; Site_2:

XhoI; Cloned unidirectionally. Primer: Oligo dt. Uni-ZAP

XR vector. Average insert size: 1.5kb.; 5' adaptor

sequence: 5' GAATTCGACGACGAG 3'; 3' adaptor sequence: 5'

CTCGAGTTTCTTTTCTTTTCTTTT 3'"

ORIGIN

Alignment Scores:
Pred. No.: 320 Length: 413
Score: 46.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 66.67% Indels: 0
DB: 1 Gaps: 0

US-09-857-841-4 (1-14) x AL584972 (1-413)

Qy 1 MetaplyserGluSerTherSerAlaGlyArgAsnArg 14

Db 267 ATACGAAATCTGAAGTACAGCTCTGAAACACACGCGG 226

RESULT 10

AL836204

LOCUS ALB36204 480 bp mRNA linear EST 27-FEB-2004
DEFINITION ALB36204 EFRd Takifugu rubripes cDNA clone EFRd002apA11, mRNA
SEQUENCE.
ACCESSION ALB36204
VERSION ALB36204.1 GI:21878166
KEYWORDS EST.
SOURCE Takifugu rubripes (Fugu rubripes)
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Takifugu.
1 (bases 1 to 480)
Clark, M.S., Edwards, Y.Y., Peterson, D., Clifton, S.W., Thompson, A.J.,
Sasaki, M., Suzuki, Y., Kikuchi, K., Matabe, S., Kawakami, K.,
Sugano, S., Elgar, G. and Johnson, S.L.
Fugu ESTs: new resources for transcription analysis and genome
annotation
Genome Res. 13 (12), 2747-2753 (2003)
CONTACT: Clark MS
MRC Human Genome Mapping Project Resource Centre
Hinxton, Cambridge, CB10 1SB, UK
Email: biohelp@hgm.mrc.ac.uk
Email: biohelp@hgm.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
The clone can be obtained from www.hgm.mrc.ac.uk
Library created by Greg Elgar
MRC Human Genome Mapping Project Resource Centre, Hinxton,
Cambridge, CB10 1SB, UK
Library sequenced by Sarah Warner and Jim Hills
MRC Human Genome Mapping Project Resource Centre, Hinxton,
Cambridge, CB10 1SB, UK
Location/Qualifiers
1. 480
/organism="Takifugu rubripes"
/mol_type="mRNA"
/db_xref="taxon:31033"
/clone="EFRd002apA11"
/cissue_type="gut"
/clone_lib="EFRd"
/note="Vector: pBluescript II KS"

ORIGIN
Alignment Scores:
Pred. No.: 373 Length: 480
Score: 46.00 Matches: 10
Percent Similarity: 76.92% Conservative: 0
Best Local Similarity: 76.92% Mismatches: 3
Query Match: 66.67% Indels: 0
DB: 1 Gaps: 0
US-09-857-841-4 (1-14) x ALB36204 (1-480)

CY 2 AsplyserGluSerThrSerAlaGlyArgAsnArg 14
DB 397 GATGGAGCGAATCGAAGCGCTCGACGACACCA 435
RESULT 11
LOCUS BX256743/c
DEFINITION BX256743 486 bp mRNA linear EST 24-MAY-2004
SEQUENCE.
ACCESSION BX256743
VERSION BX256743.2 GI:47581535
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 486)
AUTHORS Herault, F., Le Meuth-Metzinger, V., Desert, C., Retout, E., Piumi, F.,
Klopp, C. and Donaire, M.
TITLE Construction and primary characterization of chicken normalized
multi-tissue cDNA libraries
JOURNAL Unpublished (2003)
COMMENT On Feb 27, 2003 this sequence version replaced gi:28579341.
CONTACT: Donaire M
INRA, UMR INRA-ENSAT Genetique Animale
65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE
Tel: +33 (0) 2.23.48.54.63
Fax: +33 (0) 2.23.48.54.70
Email: Madeleine.Donaire@roazhon.inra.fr
at sequence cleaned of vector, adaptor and repetitions. Contact us
at senesupport@jouy.inra.fr to obtain the chromatogram of this
sequence
Plate: 0001 row: c column: 5
Seq primer: M13R.
Location/Qualifiers
1. 486
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="gcag0001c.c.05"
/cissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="AGENAE Gallus gallus multi-tissues normalized
library (gcag)"
/note="Vector: pT7T3D-pac; tissues: brain, embryos,
kidney, multi-tissues, muscle, pancreas, skin, testis,
liver, adipose tissue, granulosa, utero-vaginal gland,
oviduct, small intestine, ovary, hypothalamus, pituitary
gland, ileum, jejunum, caecum, duodenum, spleen,
fabricius gland, bone marrow, thymus, hematopoietic
progenitor cells. Clone distribution: AGENAE Resource
centre, Francois Piumi, Francois Piumi, Inra.fr, INRA, CEA
Radiobiologie et Etude du genome (LREG), Domaine de
Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"

ORIGIN
Alignment Scores:
Pred. No.: 378 Length: 486
Score: 46.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 66.67% Indels: 0
DB: 5 Gaps: 0
US-09-857-841-4 (1-14) x BX256743 (1-486)

CY 1 MetAsplyserGluSerThrSerAlaGlyArgAsnArg 14
DB 71 ATACGAAATCTGAAGTACGCTCTGAAACACAGCGCG 30
RESULT 12
LOCUS BX256742/c
DEFINITION BX256742 490 bp mRNA linear EST 24-MAY-2004
SEQUENCE.
ACCESSION BX256742
VERSION BX256742.2 GI:47581534
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 490)
Herault, F., Le Meuth-Metzinger, V., Desert, C., Retout, E., Piumi, F.,
Klopp, C. and Donaire, M.
TITLE Construction and primary characterization of chicken normalized

JOURNAL
COMMENT

multi-tissue cDNA libraries
Unpublished (2003)
On Feb 27, 2003 this sequence version replaced gi:28579340.
Contact: Douaire M
INRA, UMR INRA-ENSAR Genetique Animale
65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE
Tel: +33 (0) 2.23.48.54.63
Fax: +33 (0) 2.23.48.54.70
Email: Madeleine.Douaire@roazon.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at ajgenesupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0001 row: c column: 5
Seq primer: M13P.

FEATURES

SOURCE

Location/Qualifiers

1..490
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="gcag0001c.c.05"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="AGENAE Gallus gallus multi-tissues normalized
library (gcag)"
/note="Vector: pRTT3D-pac; tissues: brain, embryos,
kidney, multi-tissues, muscle, pancreas, skin, testis,
liver, adipose tissue, granulosa, utero-vaginal gland,
oviduct, small intestine, caecum, duodenum, spleen,
gland, ileum, jejunum, ovary, hypothalamus, pituitary
gland, bone marrow, thymus, hematopoietic
progenitor cells. Clone distribution: AGENAE Resource
centre: Francois PIUMI, Francois.PIUMI.inra.fr, INRA, CEA
Radiobiologie et Etude du genome (LREB), Domaine de
Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"

ORIGIN

Alignment Scores:

Pred. No.: 381 Length: 490
Score: 46.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 66.67% Indels: 0
DB: 5 Gaps: 0

US-09-857-841-4 (1-14) x BK256742 (1-490)

Qy 1 MetaplysSerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 71 ATACGAAATCTGAAAGTACACGCTCTCGAAACACACGCGG 30

RESULT 13
CD356033 645 bp mRNA linear EST 29-MAY-2003
LOCUS CD356033
DEFINITION IMAGE30379119 5', mRNA sequence.

ACCESSION CD356033
VERSION CD356033.1 GI:31127444
KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 645)
TITLE NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein

FEATURES

SOURCE

CDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLU)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLU at:
<http://image.lnl.gov>
Plate: NDCM169 row: a column: 16
High quality sequence stop: 258.

Location/Qualifiers

1..645
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30379119"
/lab_host="DH10B (rti-phage-resistant)"
/clone_lib="NIH_MGC_176"
/note="Organ: Kidney; Vector: pDNR-LIB, Site 1: SfiI
(ggccatcggcc); Site 2: SfiI (ggccgcctcgcc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTCATACGACGACGACGACATG-dt(30)NN-3'. Full-length
5'-ATTCTAGAGCCGAGGCGCGGACATG-dt(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 505 Length: 645
Score: 46.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 66.67% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x CD356033 (1-645)

Qy 1 MetaplysSerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 112 CTTTCAAAACAGAGGCGGTTCGTGGAGAAACCGCGCA 153

RESULT 14
CF577172

LOCUS CF577172 653 bp mRNA linear EST 24-SEP-2003
DEFINITION MCSA209604 Maturing Sugarcane Stem Lambda ZIPPOX Library (MCS)

ACCESSION CF577172
VERSION CF577172.1 GI:35208498
KEYWORDS EST.

SOURCE Saccharum sp.
ORGANISM Saccharum sp.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Saccharum.
1 (bases 1 to 653)
TITLE Casu,R.E., Dimmock,C.M., Chapman,S.C., Grof,C.P.L., McIntyre,C.L.,
Bonnett,G.D. and Manners,J.M.

Identification of differentially expressed transcripts from
maturing stem of sugarcane by in silico analysis of stem expressed
sequence tags and gene expression profiling
Unpublished (2003)
Contact: Rosanne E. Casu
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
Long Pocket Laboratories, 120 Meiers Rd, Indooroopilly, QLD, 4068,
Australia

JOURNAL

COMMENT

Unpublished (2003)
Contact: Rosanne E. Casu
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
Long Pocket Laboratories, 120 Meiers Rd, Indooroopilly, QLD, 4068,
Australia
Tel: 61 7 3214 2364
Fax: 61 7 3214 2881
Email: Rosanne.Casu@csiro.au
Bases 1-17 (GTGACCCACGCGCCG): Sali adapter
Seq primer: T7 sequencing primer
High quality sequence stop: 655.

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 5, 2004, 08:19:02 ; Search time 67 Seconds
(without alignments)
148.523 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDKSESTSGAGNRR 14

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.epool/US09857841/runat_03122004.160552.18608/app_query.fasta_1.199
-DB=Issued Patents NA -QEMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MILEN=0 -MAXLEN=2000000000
-USER=US09857841.qcgn2_1.1.69 @runat_03122004.160552.18608 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOUDRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELop=6 -DELext=7

Database :

Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 69 | 100.0 | 130 | 1 | US-08-090-193-14 |
| 2 | 69 | 100.0 | 130 | 2 | US-08-488-031-11 |
| 3 | 69 | 100.0 | 130 | 2 | US-08-488-031-11 |
| 4 | 69 | 100.0 | 130 | 2 | US-08-488-031-11 |
| 5 | 69 | 100.0 | 130 | 2 | US-08-488-031-11 |
| 6 | 69 | 100.0 | 130 | 2 | US-08-488-031-11 |
| 7 | 69 | 100.0 | 130 | 2 | US-08-488-031-11 |
| 8 | 69 | 100.0 | 130 | 2 | US-08-488-031-11 |
| 9 | 69 | 100.0 | 130 | 2 | US-08-488-031-11 |
| 10 | 69 | 100.0 | 130 | 2 | US-08-488-031-11 |
| 11 | 69 | 100.0 | 130 | 2 | US-08-488-031-11 |
| 12 | 69 | 100.0 | 130 | 2 | US-08-488-031-11 |

| | | | | | | |
|----|----|-------|-----|---|------------------|-------------------|
| 13 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 14 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 15 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 16 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 17 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 18 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 19 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 20 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 21 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 22 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 23 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 24 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 25 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 26 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 27 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 28 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 29 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 30 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 31 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 32 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 33 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 34 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 35 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 36 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 37 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 38 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 39 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 40 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 41 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 42 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 43 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 44 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 45 | 69 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |

ALIGNMENTS

RESULT 1
US-08-090-193-14
Sequence 14, Application US/08090193
Patent No. 5641673
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Pettimon, No. 5641673bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESS: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,193
FILING DATE: 23-DEC-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0609.3080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-090-193-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-857-841-4 (1-14) x US-08-090-193-14 (1-130)

QY 1 MetApLySeSerGIuSerThrSerAlaGlyArgGlnArg 14
Db 53 ATGACAAATCTGATCAACACGAGTGTGTCGTACCGTGA 94

RESULT 2
US-08-488-031-14
Sequence 14, Application US/08488031
Patent No. 5849548
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5849548bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,031
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080002/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both

TOPOLOGY: linear
US-08-488-031-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-031-14 (1-130)

QY 1 MetApLySeSerGIuSerThrSerAlaGlyArgGlnArg 14
Db 53 ATGACAAATCTGATCAACACGAGTGTGTCGTACCGTGA 94

RESULT 3
US-08-486-569-14
Sequence 14, Application US/08486569
Patent No. 5863774
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5863774bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,569
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080006/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-486-569-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-486-563-14 (1-130)

QY 1 MetaplyseSerGluSerThrSerAlaGlyArgAsnArg 14
Db 53 ATGACAAATCTGATCAACCAAGCTGCTGTGTAACCTGCA 94

RESULT 4

US-08-488-027-14

Sequence 14, Application US/08488027

Patent No. 5866384

GENERAL INFORMATION:

APPLICANT: Haseloff, James

APPLICANT: Brand, Andrea

APPLICANT: Perrimon, No. 5866384bert

APPLICANT: Goodman, Howard M.

TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,027

FILING DATE: 07-JUN-1995

PRIOR APPLICATION NUMBER: 08/090,193

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/00277

FILING DATE: 16-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/642,330

FILING DATE: 17-JAN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Bugalsky, Lawrence B.

REGISTRATION NUMBER: 35,086

REFERENCE/DOCKET NUMBER: 0609.3080003/MAC/LBB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 130 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

US-08-488-027-14

Alignment Scores:

Pred. No.: 0.00013 Length: 130

Score: 69.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-027-14 (1-130)

QY 1 MetaplyseSerGluSerThrSerAlaGlyArgAsnArg 14
Db 53 ATGACAAATCTGATCAACCAAGCTGCTGTGTAACCTGCA 94

RESULT 5

US-08-090-192-14

Sequence 14, Application US/08090192

Patent No. 5874414

GENERAL INFORMATION:

APPLICANT: Haseloff, James

APPLICANT: Goodman, Howard M.

TITLE OF INVENTION: Trans-Splicing Ribozymes

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/090,192

FILING DATE: 11-NOV-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/ US 92/00278

FILING DATE: 16-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/642,333

FILING DATE: 17-JAN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Cimbal, Michele A.

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0609.3030001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 130 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

US-08-090-192-14

Alignment Scores:

Pred. No.: 0.00013 Length: 130

Score: 69.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-090-192-14 (1-130)

QY 1 MetaplyseSerGluSerThrSerAlaGlyArgAsnArg 14
Db 53 ATGACAAATCTGATCAACCAAGCTGCTGTGTAACCTGCA 94

RESULT 6

US-08-482-663-14

Sequence 14, Application US/08482663

Patent No. 5882907

GENERAL INFORMATION:

APPLICANT: Haseloff, James

APPLICANT: Brand, Andrea

APPLICANT: Perrimon, No. 5882907bert

APPLICANT: Goodman, Howard M.

TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,663
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080005/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-482-663-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-482-663-14 (1-130)
OY 1 MetApLySeRgUSeRThSeRAlaGlyARgAsnARgArg 14
Db 53 ATGGACAAATCTGATCAACCAAGTCGTGCTGTAACCTCGA 94

RESULT 7
US-08-482-658-14
Sequence 14, Application US/08482658
Patent No. 6010904
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Peritmon, No. 6010904bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080008/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-482-658-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-857-841-4 (1-14) x US-08-482-658-14 (1-130)
OY 1 MetApLySeRgUSeRThSeRAlaGlyARgAsnARgArg 14
Db 53 ATGGACAAATCTGATCAACCAAGTCGTGCTGTAACCTCGA 94

RESULT 8
US-08-470-349-14
Sequence 14, Application US/08470349
Patent No. 6015794
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,349
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,192
FILING DATE: 11-NOV-1993
APPLICATION NUMBER: PCT/ US 92/00278
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,333

FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-470-349-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-857-841-4 (1-14) x US-08-470-349-14 (1-130)

Cy 1 MetApLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 53 ATGGCAATCTGAATCAACGAGTCTGTCGTACCGTCGA 94

RESULT 9
US-08-475-610-14
Sequence 14, Application US/08475610
Patent No. 6071730
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perlmom, No. 6071730bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,610
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080004/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-475-610-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-857-841-4 (1-14) x US-08-475-610-14 (1-130)

Cy 1 MetApLySerGluSerThrSerAlaGlyArgAsnArgArg 14
Db 53 ATGGCAATCTGAATCAACGAGTCTGTCGTACCGTCGA 94

RESULT 10
PCT-US92-00277-14
Sequence 14, Application PC/TUS9200277
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
APPLICANT: Brand, Andrea
APPLICANT: Perlmom, Norbert
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 19920116
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3496604
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)833-7533
TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US92-00277-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-857-841-4 (1-14) x PCT-US92-00277-14 (1-130)

OY 1 MetaplySergJuserThSerAlaGlyArgAnaArg 14
DB 53 ATGACAAATCTGAATCAACAGTCTGCTGTAACCTGCA 94

RESULT 11
PCT-US92-00278-14

Sequence 14, Application PC/TUS9200278
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00278
FILING DATE: 19920116
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 07/642,333
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3476604
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)833-7533
TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Nucleic Acid
PCT-US92-00278-14

Alignment Scores:
Pred. No.: 0.00013 Length: 130
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-857-841-4 (1-14) x PCT-US92-00278-14 (1-130)

OY 1 MetaplySergJuserThSerAlaGlyArgAnaArg 14
DB 53 ATGACAAATCTGAATCAACAGTCTGCTGTAACCTGCA 94

RESULT 12

US-08-090-193-11
Sequence 11, Application US/08090193
Patent No. 5641673
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5641673bert
APPLICANT: Goodman, Howard M.

TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,193
FILING DATE: 23-DEC-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-090-193-11

Alignment Scores:
Pred. No.: 0.00013 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-857-841-4 (1-14) x US-08-090-193-11 (1-131)

OY 1 MetaplySergJuserThSerAlaGlyArgAnaArg 14
DB 54 ATGACAAATCTGAATCAACAGTCTGCTGTAACCTGCA 95

RESULT 13
US-08-488-031-11
Sequence 11, Application US/08488031
Patent No. 5849548
GENERAL INFORMATION:

APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5849548bert
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,031
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080002/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-488-031-11

Alignment Scores:
Pred. No.: 0.000131 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 2

US-09-857-841-4 (1-14) x US-08-488-031-11 (1-131)
Qy 1 MetAplySergJuserThSerAlaGlyArgAsnArg 14
Db 54 ATGACCAATCTGATCAACACGAGTCTGCTGTAACCTCGA 95

RESULT 14
US-08-486-569-11
Sequence 11, Application US/08486569
Patent No. 5863774
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5863774bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,569
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080006/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-486-569-11

Alignment Scores:
Pred. No.: 0.000131 Length: 131
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 2

US-09-857-841-4 (1-14) x US-08-486-569-11 (1-131)
Qy 1 MetAplySergJuserThSerAlaGlyArgAsnArg 14
Db 54 ATGACCAATCTGATCAACACGAGTCTGCTGTAACCTCGA 95

RESULT 15
US-08-488-027-11
Sequence 11, Application US/08488027
Patent No. 586384
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 586384bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,027
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086

REFERENCE/DOCKET NUMBER: 0609.3080003/MAC/LBB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 131 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 US-08-488-027-11

Alignment Scores:
 Pred. No.: 0.000131 Length: 131
 Score: 69.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-027-11 (1-131)

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 Db 54 ATGACAAATCTGATCAACCAAGTCTGTCTTAACCGTCGA 95

Search completed: December 5, 2004, 09:48:23
 Job time : 68 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: December 5, 2004, 08:17:52 ; Search time 350 Seconds

(without alignments)
219.793 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 69
Sequence: 1 MDSEESTSAGNRNR 14

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 3694831 seqs, 2747406616 residues
Total number of hits satisfying chosen parameters: 7389662

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications NA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 3 | 69 | 100.0 | 772 | 13 US-10-011-033-14 | Sequence 14, Appl1 |
| 4 | 69 | 100.0 | 792 | 13 US-10-011-033-3 | Sequence 3, Appl1 |
| 5 | 64 | 92.8 | 960 | 13 US-10-011-033-9 | Sequence 9, Appl1 |
| 6 | 48 | 69.6 | 3048 | 18 US-10-425-115-175381 | Sequence 176381, |
| 7 | 47 | 68.1 | 609 | 17 US-10-437-963-2533 | Sequence 2533, Ap |
| 8 | 47 | 68.1 | 792 | 17 US-10-437-963-3120 | Sequence 3120, Ap |
| 9 | 45 | 65.2 | 297 | 17 US-10-437-963-63644 | Sequence 63644, A |
| 10 | 44 | 63.8 | 568 | 17 US-10-437-963-49610 | Sequence 49610, A |
| 11 | 44 | 63.8 | 571 | 17 US-10-437-963-92187 | Sequence 92187, A |
| 12 | 44 | 63.8 | 615 | 17 US-10-437-963-64563 | Sequence 64563, A |
| 13 | 44 | 63.8 | 1603 | 16 US-10-282-122A-26385 | Sequence 26385, A |
| 14 | 43 | 62.3 | 2625 | 16 US-10-282-122A-28450 | Sequence 28450, A |
| 15 | 43 | 62.3 | 969 | 17 US-10-437-963-86635 | Sequence 86635, A |
| 16 | 43 | 62.3 | 1014 | 17 US-10-437-963-64807 | Sequence 64807, A |
| 17 | 43 | 62.3 | 2377 | 18 US-10-425-115-176349 | Sequence 176349, |
| 18 | 43 | 62.3 | 2979 | 18 US-10-425-115-176386 | Sequence 176386, |
| 19 | 43 | 62.3 | 3105 | 18 US-10-425-115-86212 | Sequence 86212, A |
| 20 | 43 | 62.3 | 3175 | 18 US-10-425-115-176380 | Sequence 176380, |
| 21 | 43 | 62.3 | 125439 | 17 US-10-450-826-84 | Sequence 84, Appl1 |
| 22 | 42 | 60.9 | 358 | 11 US-09-987-899-2205 | Sequence 2205, Ap |
| 23 | 42 | 60.9 | 380 | 18 US-10-425-115-63116 | Sequence 63116, A |
| 24 | 42 | 60.9 | 414 | 17 US-10-437-963-15259 | Sequence 15259, A |
| 25 | 42 | 60.9 | 559 | 17 US-10-437-963-32355 | Sequence 32355, A |
| 26 | 42 | 60.9 | 610 | 15 US-10-027-632-717 | Sequence 717, App |
| 27 | 42 | 60.9 | 610 | 15 US-10-027-632-717 | Sequence 717, App |
| 28 | 42 | 60.9 | 889 | 17 US-10-437-963-34410 | Sequence 34410, A |
| 29 | 42 | 60.9 | 1058 | 16 US-10-424-599-113581 | Sequence 113581, |
| 30 | 42 | 60.9 | 1068 | 17 US-10-437-963-93102 | Sequence 93102, A |
| 31 | 42 | 60.9 | 1073 | 18 US-10-425-115-20144 | Sequence 20144, A |
| 32 | 42 | 60.9 | 1267 | 16 US-10-305-720-1267 | Sequence 1267, Ap |
| 33 | 42 | 60.9 | 1506 | 17 US-10-437-963-97456 | Sequence 97456, A |
| 34 | 42 | 60.9 | 1746 | 13 US-10-001-843-35 | Sequence 35, Appl1 |
| 35 | 42 | 60.9 | 1825 | 17 US-10-437-963-93100 | Sequence 93100, A |
| 36 | 42 | 60.9 | 1942 | 17 US-09-800-274-1 | Sequence 1, Appl1 |
| 37 | 42 | 60.9 | 2900 | 15 US-10-425-567A-23 | Sequence 23, Appl1 |
| 38 | 42 | 60.9 | 29283 | 17 US-10-741-601-5720 | Sequence 5720, Ap |
| 39 | 41.5 | 60.1 | 2508 | 17 US-10-437-963-60204 | Sequence 60204, A |
| 40 | 41 | 59.4 | 243 | 17 US-10-437-963-89248 | Sequence 89248, A |
| 41 | 41 | 59.4 | 289 | 9 US-09-284-093B-1361 | Sequence 1361, Ap |
| 42 | 41 | 59.4 | 385 | 18 US-10-425-115-134580 | Sequence 134580, |
| 43 | 41 | 59.4 | 523 | 18 US-10-425-115-79864 | Sequence 79864, A |
| 44 | 41 | 59.4 | 563 | 16 US-10-424-599-31741 | Sequence 31741, A |
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ALIGNMENTS

RESULT 1
US-10-011-033-5
; Sequence 5, Application US/10011033
; Publication No. US20020124286A1

GENERAL INFORMATION:

APPLICANT: Boehringer, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J

TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.

STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60689
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber mosaic virus
STRAIN: V-34
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
OTHER INFORMATION: /codon_start=3
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US-10-011-033-5
Alignment Scores:
Pred. No.: 0.00072 Length: 771
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 13
US-09-857-841-4 (1-14) x US-10-011-033-5 (1-771)
QY 1 MetApLySeRgIuSeRThSeRnIaG1YArGSeNaRgArG 14
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RESULT 2
US-10-011-033-1
Sequence 1, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: V-27
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-011-033-1
Alignment Scores:
Pred. No.: 0.000721 Length: 772
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 13
US-09-857-841-4 (1-14) x US-10-011-033-1 (1-772)
QY 1 MetApLySeRgIuSeRThSeRnIaG1YArGSeNaRgArG 14
Db 3 ATGGACAAATCTGAATCAACGAGTCTGTGCTAACCGTCCG 44
RESULT 3
US-10-011-033-14
Sequence 14, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: A35
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-011-033-14
Alignment Scores:
Pred. No.: 0.000721 Length: 772
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-14 (1-772)
Cy 1 MetApLySeRgUSeRThSeRnAgLyArGaSnArGArG 14
Db 3 ATGGACAAATCTGAATCAACCAAGTCGTCTGTACCGTCA 44
RESULT 4
US-10-011-033-3
Sequence 3, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: v-33
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-011-033-3
Alignment Scores:
Pred. No.: 0.000741 Length: 792
Score: 69.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-3 (1-792)
Cy 1 MetApLySeRgUSeRThSeRnAgLyArGaSnArGArG 14
Db 3 ATGGACAAATCTGAATCAACCAAGTCGTCTGTACCGTCA 44
RESULT 5
US-10-011-033-9
Sequence 9, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: STRAIN C
FEATURE:
NAME/KEY: CDS
LOCATION: 1..658
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-011-033-9

Alignment Scores:
Pred. No.: 0.00827 Length: 960
Score: 64.00 Matches: 13
Percent Similarity: 92.86% Conservative: 0
Best Local Similarity: 92.86% Mismatches: 1
Query Match: 92.75% Indels: 0
DB: 13 Gaps: 0

US-09-857-841-4 (1-14) x US-10-011-033-9 (1-960)

Oy 1 MetApIysSerGluSerThrSerAlaGlyArgAsnArg 14
DB 1 ATGGACAAATCTGAATCAACCAAGTCTGCTGAACATCA 42

RESULT 6
US-10-425-115-176381
Sequence 176381, Application US/10425115
Publication NO. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 176381
LENGTH: 3048
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_92452C.1
US-10-425-115-176381

Alignment Scores:
Pred. No.: 32.9 Length: 3048
Score: 48.00 Matches: 8
Percent Similarity: 85.71% Conservative: 4
Best Local Similarity: 57.14% Mismatches: 2
Query Match: 69.57% Indels: 0
DB: 18 Gaps: 0

US-09-857-841-4 (1-14) x US-10-425-115-176381 (1-3048)

Oy 1 MetApIysSerGluSerThrSerAlaGlyArgAsnArg 14
DB 1034 CTGGACAAAGCAGACGCGCTGGGAAAGAAACCGCGG 1075

RESULT 7
US-10-437-963-2533/C
Sequence 2533, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 2533
LENGTH: 609
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_102297C.1
US-10-437-963-2533

Alignment Scores:
Pred. No.: 9.37 Length: 609
Score: 47.00 Matches: 9
Percent Similarity: 84.62% Conservative: 2
Best Local Similarity: 69.23% Mismatches: 2
Query Match: 68.12% Indels: 0
DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-2533 (1-609)

Oy 2 AspIysSerGluSerThrSerAlaGlyArgAsnArg 14
DB 440 GACAAAGCCAGACGACCTCCGCCGCAAGAAATGCCGC 402

RESULT 8
US-10-437-963-3120
Sequence 3120, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 3120
LENGTH: 792
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_102831C.1
US-10-437-963-3120

Alignment Scores:
Pred. No.: 12.4 Length: 792
Score: 47.00 Matches: 10
Percent Similarity: 90.91% Conservative: 0

Best Local Similarity: 90.91% Mismatches: 1
Query Match: 68.12% Indels: 0
DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-3120 (1-792)

QY 4 SerGluSerThSerAlaGlyArgAsnArg 14
|||||
DB 734 TCGAGAGCACCCTGCGCGCGCGCGCGCT 766

RESULT 9
US-10-437-963-63644/C
; Sequence 63644, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 63644
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_64867C.1
US-10-437-963-63644

Alignment Scores:
Pred. No.: 10.6 Length: 297
Score: 45.00 Matches: 9
Percent Similarity: 84.62% Conservative: 2
Best Local Similarity: 69.23% Mismatches: 2
Query Match: 65.22% Indels: 0
DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-63644 (1-297)

QY 2 AspGluSerGluSerThSerAlaGlyArgAsnArg 14
|||||
DB 175 GACAAAGCGGAGCAGCCTCGCGCGCGCAAGATGCGCGC 137

RESULT 10
US-10-437-963-49610/C
; Sequence 49610, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 49610
; LENGTH: 568
; TYPE: DNA

; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52178C.1
US-10-437-963-49610

Alignment Scores:
Pred. No.: 32.8 Length: 568
Score: 44.00 Matches: 8
Percent Similarity: 84.62% Conservative: 3
Best Local Similarity: 61.54% Mismatches: 2
Query Match: 63.77% Indels: 0
DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-49610 (1-568)

QY 2 AspGluSerGluSerThSerAlaGlyArgAsnArg 14
|||||
DB 395 GACAAAGCGGAGCAGCAGCGCGCGCAAGATGCGCGC 357

RESULT 11
US-10-437-963-92187/C
; Sequence 92187, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 92187
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_90693C.1
US-10-437-963-92187

Alignment Scores:
Pred. No.: 33 Length: 571
Score: 44.00 Matches: 8
Percent Similarity: 84.62% Conservative: 3
Best Local Similarity: 61.54% Mismatches: 2
Query Match: 63.77% Indels: 0
DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-92187 (1-571)

QY 2 AspGluSerGluSerThSerAlaGlyArgAsnArg 14
|||||
DB 380 GACAAAGCGGAGCAGCAGCGCGCGCAAGATGCGCGC 342

RESULT 12
US-10-437-963-64563
; Sequence 64563, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

;; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;; FILE REFERENCE: 38-21(53221)B
;; CURRENT APPLICATION NUMBER: US/10/437,963
;; CURRENT FILING DATE: 2003-05-14
;; NUMBER OF SEQ ID NOS: 204966
;; SEQ ID NO 64563
;; LENGTH: 615
;; TYPE: DNA
;; ORGANISM: Oryza sativa
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MRT4530_65695C.1
US-10-437-963-64563

Alignment Scores:
Pred. No.: 35.6 Length: 615
Score: 44.00 Matches: 8
Percent Similarity: 84.62% Conservative: 3
Best Local Similarity: 61.54% Mismatches: 2
Query Match: 63.77% Indels: 0
DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-64563 (1-615)

Oy 2 AspySerGIuSerThSerAlaGIyArGaAnArgArg 14
Db 170 GACAAAGCCAGGACGACGACCGCCGCAAGAAATGCCGCC 208

RESULT 13
US-10-282-122A-26385/c
;; Sequence 26385, Application US/10282122A
;; Publication No. US20040029129A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Liangsu
;; APPLICANT: Zamudio, Carlos
;; APPLICANT: Malone, Cheryl
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Kari
;; APPLICANT: Zykied, Judith
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John
;; APPLICANT: Carr, Grant
;; APPLICANT: Yamamoto, Robert
;; APPLICANT: Forsyth, R.
;; APPLICANT: Xu, H.
;; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;; FILE REFERENCE: ELITRA.034A
;; CURRENT APPLICATION NUMBER: US/10/282,122A
;; CURRENT FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 26385

;; LENGTH: 1603
;; TYPE: DNA
;; ORGANISM: Mycobacterium bovis
US-10-282-122A-26385

Alignment Scores:
Pred. No.: 97.9 Length: 1603
Score: 44.00 Matches: 9
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 63.77% Indels: 0
DB: 16 Gaps: 0

US-09-857-841-4 (1-14) x US-10-282-122A-26385 (1-1603)

Oy 3 LysSerGIuSerThSerAlaGIyArGaAnArgArg 14
Db 1240 CGCCAGATCGACTTCGCGGCGGCGGTGGAAGA 1205

RESULT 14
US-10-282-122A-28450/c
;; Sequence 28450, Application US/10282122A
;; Publication No. US20040029129A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Liangsu
;; APPLICANT: Zamudio, Carlos
;; APPLICANT: Malone, Cheryl
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Kari
;; APPLICANT: Zykied, Judith
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John
;; APPLICANT: Carr, Grant
;; APPLICANT: Yamamoto, Robert
;; APPLICANT: Forsyth, R.
;; APPLICANT: Xu, H.
;; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;; FILE REFERENCE: ELITRA.034A
;; CURRENT APPLICATION NUMBER: US/10/282,122A
;; CURRENT FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 28450
;; LENGTH: 2625
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-28450

Alignment Scores:
Pred. No.: 165 Length: 2625
Score: 44.00 Matches: 9
Percent Similarity: 83.33% Conservative: 1

Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 63.77% Indels: 0
 DB: 16 Gaps: 0

US-09-857-841-4 (1-14) x US-10-282-122A-28450 (1-2625)

Qy 3 LysSerGluSerThrSerAlaGlyArgAsnArg 14
 Db 1273 CGCCGAGATTCTGACAAACACCGCGCGCGCTCGAAGA 1238

RESULT 15

US-10-437-963-86635/c
 ; Sequence 86635, Application US/10437963
 ; Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Mu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barabazuk, Brad
 APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 86635

LENGTH: 969

TYPE: DNA

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT4530_85657C.1

US-10-437-963-86635

Alignment Scores:

| Pred. No.: | 89.6 | Length: | 969 |
|------------------------|--------|---------------|-----|
| Score: | 43.00 | Matches: | 8 |
| Percent Similarity: | 78.57% | Conservative: | 3 |
| Best Local Similarity: | 57.14% | Mismatches: | 3 |
| Query Match: | 62.32% | Indels: | 0 |
| DB: | 17 | Gaps: | 0 |

US-09-857-841-4 (1-14) x US-10-437-963-86635 (1-969)

Qy 1 MetAspLysSerGluSerThrSerAlaGlyArgAsnArg 14
 Db 915 ATGTGCAATTCTGACAAACACCGCGCGCGCTCGA 874

Search completed: December 5, 2004, 09:47:10
 Job time : 351 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 09:07:08 ; Search time 2542 Seconds

(without alignments)
260.447 Million cell updates/sec

Title: US-09-857-841-4

Sequence: 1 MDKSESTAGNNR 14

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 segs, 23644849745 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9041059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09857841/runat_03122004_160613_19119/app_query.fasta.1.199
-DB=GenBml -QMT=fastap -SUFFIX=olip2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco
-NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

GenBml:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sets:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 14 | 100.0 | 53 | 6 | BD261798 |
| 2 | 14 | 100.0 | 130 | 6 | AR031575 Sequence |
| 3 | 14 | 100.0 | 130 | 6 | AR065687 Sequence |
| 4 | 14 | 100.0 | 130 | 6 | AR097446 Sequence |

| | | | | | | |
|----|----|-------|-----|----|----------|--------------------|
| 5 | 14 | 100.0 | 130 | 6 | 149964 | 149964 Sequence 14 |
| 6 | 14 | 100.0 | 131 | 6 | AR031572 | AR031572 Sequence |
| 7 | 14 | 100.0 | 131 | 6 | AR065684 | AR065684 Sequence |
| 8 | 14 | 100.0 | 131 | 6 | AR097443 | AR097443 Sequence |
| 9 | 14 | 100.0 | 131 | 6 | 149961 | 149961 Sequence 11 |
| 10 | 14 | 100.0 | 152 | 6 | AR031570 | AR031570 Sequence |
| 11 | 14 | 100.0 | 152 | 6 | AR031571 | AR031571 Sequence |
| 12 | 14 | 100.0 | 152 | 6 | AR065682 | AR065682 Sequence |
| 13 | 14 | 100.0 | 152 | 6 | AR065683 | AR065683 Sequence |
| 14 | 14 | 100.0 | 152 | 6 | AR097441 | AR097441 Sequence |
| 15 | 14 | 100.0 | 152 | 6 | AR097442 | AR097442 Sequence |
| 16 | 14 | 100.0 | 152 | 6 | 149959 | 149959 Sequence 9 |
| 17 | 14 | 100.0 | 152 | 6 | 149960 | 149960 Sequence 10 |
| 18 | 14 | 100.0 | 154 | 6 | AR031573 | AR031573 Sequence |
| 19 | 14 | 100.0 | 154 | 6 | AR031574 | AR031574 Sequence |
| 20 | 14 | 100.0 | 154 | 6 | AR065685 | AR065685 Sequence |
| 21 | 14 | 100.0 | 154 | 6 | AR065686 | AR065686 Sequence |
| 22 | 14 | 100.0 | 154 | 6 | AR097444 | AR097444 Sequence |
| 23 | 14 | 100.0 | 154 | 6 | AR097445 | AR097445 Sequence |
| 24 | 14 | 100.0 | 154 | 6 | 149962 | 149962 Sequence 12 |
| 25 | 14 | 100.0 | 154 | 6 | 149963 | 149963 Sequence 13 |
| 26 | 14 | 100.0 | 654 | 6 | E01760 | E01760 DNA encodin |
| 27 | 14 | 100.0 | 654 | 6 | AF444252 | AF444252 Banana mo |
| 28 | 14 | 100.0 | 657 | 14 | AB070622 | AB070622 Cucumbe |
| 29 | 14 | 100.0 | 657 | 14 | AB109909 | AB109909 Cucumbe |
| 30 | 14 | 100.0 | 657 | 14 | AF198622 | AF198622 Cucumbe |
| 31 | 14 | 100.0 | 657 | 14 | AF281864 | AF281864 Cucumbe |
| 32 | 14 | 100.0 | 657 | 14 | AF316362 | AF316362 Cucumbe |
| 33 | 14 | 100.0 | 657 | 14 | AF350450 | AF350450 Cucumbe |
| 34 | 14 | 100.0 | 657 | 14 | AF368192 | AF368192 Cucumbe |
| 35 | 14 | 100.0 | 657 | 14 | AF523339 | AF523339 Cucumbe |
| 36 | 14 | 100.0 | 657 | 14 | AF523340 | AF523340 Cucumbe |
| 37 | 14 | 100.0 | 657 | 14 | AF523341 | AF523341 Cucumbe |
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| 40 | 14 | 100.0 | 657 | 14 | AF523344 | AF523344 Cucumbe |
| 41 | 14 | 100.0 | 657 | 14 | AF523345 | AF523345 Cucumbe |
| 42 | 14 | 100.0 | 657 | 14 | AF523346 | AF523346 Cucumbe |
| 43 | 14 | 100.0 | 657 | 14 | AF523347 | AF523347 Cucumbe |
| 44 | 14 | 100.0 | 657 | 14 | AF523348 | AF523348 Cucumbe |
| 45 | 14 | 100.0 | 657 | 14 | AF523349 | AF523349 Cucumbe |

ALIGNMENTS

| RESULT 1 | BD261798 | 53 bp | DNA | linear | PAT 17-JUL-2003 |
|------------|---|--|-----|--------|-----------------|
| LOCUS | BD261798 | | | | |
| DEFINITION | BD261798 | Enhancement in protein production by higher plants using ubiquitin | | | |
| ACCESSION | BD261798 | or cucumber mosaic virus coating protein peptide. | | | |
| VERSION | BD261798.1 | | | | |
| KEYWORDS | JP 2002532098-A/2. | | | | |
| SOURCE | Cucumber mosaic virus | | | | |
| ORGANISM | Cucumber mosaic virus | | | | |
| REFERENCE | Cucumber mosaic virus | | | | |
| AUTHORS | 1 (bases 1 to 53) | | | | |
| TITLE | Fang, R.X., Wu, J.L. and Chen, X.Y. | | | | |
| JOURNAL | Enhancement in protein production by higher plants using ubiquitin | | | | |
| COMMENT | or cucumber mosaic virus coating protein peptide | | | | |
| | Patent: JP 2002532098-A 2 02-OCT-2002; | | | | |
| | INSTITUTE OF MOLECULAR AGRICULTURE | | | | |
| | OS Cucumber mosaic virus | | | | |
| | PN JP 2002532098-A/2 | | | | |
| | PD 02-OCT-2002 | | | | |
| | PI 11-DEC-1998 JP 2000588378 | | | | |
| | PC RONG XIANG FANG, JING LIN WU, XIAO YING CHEN | | | | |
| | CC C12N15/09, A01H5/00, C07K4/415, C07K19/00, C12N5/10, C12N15/00, PC | | | | |
| | C12N5/00 | | | | |
| | CC Enhancement in protein production by higher plants using CC | | | | |
| | ubiquitin or | | | | |
| | CC cucumber mosaic virus coating protein peptide FH Key | | | | |

FEATURES FT CDS Location/Qualifiers
source Location/Qualifiers
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/organism="Cucumber mosaic virus"
/mol_type="genomic DNA"
/db_xref="taxon:12305"
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Pred. No.: 6.9e-06 Length: 53
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-857-841-4 (1-14) x BD261798 (1-53)
RESULT 2
AR031575 130 bp DNA linear PAT 29-SEP-1999
LOCUS AR031575
DEFINITION Sequence 14 from patent US 5866384.
ACCESSION AR031575
VERSION AR031575.1 GI:5945864
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 14 02-FEB-1999;
FEATURES Location/Qualifiers
source 1..130
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/mol_type="unassigned DNA"
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Alignment Scores:
Pred. No.: 1.68e-05 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-857-841-4 (1-14) x AR031575 (1-130)
RESULT 3
AR065687 130 bp DNA linear PAT 29-SEP-1999
LOCUS AR065687
DEFINITION Sequence 14 from patent US 5849548.
ACCESSION AR065687
VERSION AR065687.1 GI:5995903
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 14 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..130

ORIGIN /organism="unknown"
/mol_type="unassigned DNA"
Alignment Scores:
Pred. No.: 1.68e-05 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-857-841-4 (1-14) x AR065687 (1-130)
RESULT 4
AR097446 130 bp DNA linear PAT 14-FEB-2001
LOCUS AR097446
DEFINITION Sequence 14 from patent US 6071730.
ACCESSION AR097446
VERSION AR097446.1 GI:12806176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 14 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..130
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/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.68e-05 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-857-841-4 (1-14) x AR097446 (1-130)
RESULT 5
I49964 130 bp DNA linear PAT 07-OCT-1997
LOCUS I49964
DEFINITION Sequence 14 from patent US 5641673.
ACCESSION I49964
VERSION I49964.1 GI:2472184
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 130)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5641673-A 14 24-JUN-1997;
FEATURES Location/Qualifiers
source 1..130
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:

Pred. No.: 1.68e-05 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x I49964 (1-130)

OY 1 MetApIySergIuSerThrSerAlaGlyArgAsnArgArg 14
DB 53 ATGGACAAATCTGAATCAACAGTGTGCTGTAACCGTCGA 94

RESULT 6
LOCUS AR031572 131 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5866384.
ACCESSION AR031572
VERSION AR031572.1 GI:5945861
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 11 02-FEB-1999;
FEATURES Location/Qualifiers
Source 1..131
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 1.69e-05 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR031572 (1-131)

OY 1 MetApIySergIuSerThrSerAlaGlyArgAsnArgArg 14
DB 54 ATGGACAAATCTGAATCAACAGTGTGCTGTAACCGTCGA 95

RESULT 7
LOCUS AR065684 131 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5849548.
ACCESSION AR065684
VERSION AR065684.1 GI:5995900
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 11 15-DEC-1998;
FEATURES Location/Qualifiers
Source 1..131
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 1.69e-05 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR065684 (1-131)

OY 1 MetApIySergIuSerThrSerAlaGlyArgAsnArgArg 14
DB 54 ATGGACAAATCTGAATCAACAGTGTGCTGTAACCGTCGA 95

RESULT 8
LOCUS AR097443 131 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6071730.
ACCESSION AR097443
VERSION AR097443.1 GI:12806173
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 11 06-JUN-2000;
FEATURES Location/Qualifiers
Source 1..131
/organism="unknown"
/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 1.69e-05 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x AR097443 (1-131)

OY 1 MetApIySergIuSerThrSerAlaGlyArgAsnArgArg 14
DB 54 ATGGACAAATCTGAATCAACAGTGTGCTGTAACCGTCGA 95

RESULT 9
LOCUS I49961 131 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 11 from patent US 5641673.
ACCESSION I49961
VERSION I49961.1 GI:2472181
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 131)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5641673-A 11 24-JUN-1997;
FEATURES Location/Qualifiers
Source 1..131
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/mol_type="unassigned DNA"

Alignment Scores:
Pred. No.: 1.69e-05 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-857-841-4 (1-14) x I49961 (1-131)

OY 1 MetApIySergIuSerThrSerAlaGlyArgAsnArgArg 14

Db 54 ATGGACAATCTGAATCAACCAAGTCTGTCGTACCGTCGA 95
RESULT 10
LOCUS AR031570 152 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5866384.
ACCESSION AR031570
VERSION AR031570.1 GI:5945859
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 9 02-FEB-1999;
FEATURES
Location/Qualifiers
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ORIGIN
Alignment Scores:
Pred. No.: 1.96e-05 Length: 152
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-857-841-4 (1-14) x AR031571 (1-152)
Qy 1 MetApLySeRgiuSeRThSeRAlaGlyARgaNaRgArg 14
LOCUS AR031571 152 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5866384.
ACCESSION AR031571
VERSION AR031571.1 GI:5945860
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 10 02-FEB-1999;
FEATURES
Location/Qualifiers
1..152
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ORIGIN
Alignment Scores:
Pred. No.: 1.96e-05 Length: 152
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-857-841-4 (1-14) x AR031571 (1-152)
Qy 1 MetApLySeRgiuSeRThSeRAlaGlyARgaNaRgArg 14
LOCUS AR031571 152 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5866384.
ACCESSION AR031571
VERSION AR031571.1 GI:5945860
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5866384-A 10 02-FEB-1999;
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"

LOCUS AR065682 152 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5849548.
ACCESSION AR065682
VERSION AR065682.1 GI:5995898
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 9 15-DEC-1998;
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
ORIGIN
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Pred. No.: 1.96e-05 Length: 152
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-857-841-4 (1-14) x AR065682 (1-152)
Qy 1 MetApLySeRgiuSeRThSeRAlaGlyARgaNaRgArg 14
LOCUS AR065683 152 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5849548.
ACCESSION AR065683
VERSION AR065683.1 GI:5995899
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff,J., Brand,A., Perrimon,N. and Goodman,H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 5849548-A 10 15-DEC-1998;
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
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Pred. No.: 1.96e-05 Length: 152
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-857-841-4 (1-14) x AR065683 (1-152)
Qy 1 MetApLySeRgiuSeRThSeRAlaGlyARgaNaRgArg 14
LOCUS AR097441 152 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6071730.
ACCESSION AR097441
VERSION AR097441.1 GI:12806171
KEYWORDS
RESULT 14
AR097441
75 ATGGATAAATCTGAATCAACCAAGTCTGTCGTACCGTCGA 116

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 152)
AUTHORS Haseloff, J., Brand, A., Perrimon, N. and Goodman, H.M.
TITLE Cell ablation using trans-splicing ribozymes
JOURNAL Patent: US 6071730-A 9 06-JUN-2000;
FEATURES location/Qualifiers
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/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

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|------------------------|----------|---------------|-----|
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| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-09-857-841-4 (1-14) x AR097441 (1-152)

OY 1 MetApLySerGluSerThrSerAlaGlyArgAsnArgArg 14
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Db 75 ATGGACAAATCTGAATCAACGAGTCTGCTGTAACCTCGA 116
|||||

RESULT 15

AR097442

LOCUS AR097442 152 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 10 from patent US 6071730.

ACCESSION AR097442

VERSION AR097442.1 GI:12806172

KEYWORDS

SOURCE

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 152)

AUTHORS Haseloff, J., Brand, A., Perrimon, N. and Goodman, H.M.

TITLE Cell ablation using trans-splicing ribozymes

JOURNAL Patent: US 6071730-A 10 06-JUN-2000;

FEATURES location/Qualifiers

SOURCE 1..152

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

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|------------------------|----------|---------------|-----|
| Pred. No.: | 1.96e-05 | Length: | 152 |
| Score: | 14.00 | Matches: | 14 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-09-857-841-4 (1-14) x AR097442 (1-152)

OY 1 MetApLySerGluSerThrSerAlaGlyArgAsnArgArg 14
|||||
Db 75 ATGGATAATCTGAATCAACGAGTCTGCTGTAACCTCGA 116
|||||

Search completed: December 5, 2004, 10:36:25
Job time : 2542 secs

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XX Fang R, Wu J, Chen X;
PI
XX WPI: 2000-431604/37.
DR
P-PSDB; AAY90255.
XX
PT Production of desired protein in plants or plant cells by linking a
PT ubiquitin monomer coding sequence upstream of the gene encoding the
PT desired protein.
XX
PS Claim 8; Page 18; 42pp; English.
XX
CC This sequence encodes the C-terminal fragment of a ubiquitin monomer. The
CC invention relates to a method for enhancing production of a desired
CC protein in a plant or plant cell by inserting a nucleic acid (NA)
CC encoding a ubiquitin monomer upstream of a NA encoding the desired
CC protein, where the fusion construct encodes a fusion protein and
CC expression is not controlled by the ubiquitin promoter. The invention
CC also relates to a NA acid vector a NA vector able to transform a plant
CC cell, that comprises NA encoding a fusion protein having a ubiquitin
CC monomer linked to a protein of interest and further, where expression of
CC the fusion construct is not under control of a ubiquitin promoter. The
CC construct allows enhanced production of the desired protein in plants or
CC plant cells
XX
SQ Sequence 53 BP; 15 A; 14 C; 13 G; 11 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4.38e-06 Length: 53
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-857-841-4 (1-14) x AAA30858 (1-53)
OY 1 MetApLySeRgIuSeRThSeRlAgLyARgAsnARgArg 14
DB 6 ATGGACAAATCTGAATCAACGAGTGTGCTGTAACCGTCA 47
RESULT 2
AAT34666
ID AAT34666 standard; DNA; 771 BP.
AC
XX AAT34666;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the V34 strain of cucumber mosaic virus.
XX
KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KW resistance; ss.
XX
OS Cucumber mosaic virus; strain V34.
XX
FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a
XX
XX MO9621018-A1.
XX
PD 11-JUL-1996.
XX
PF 07-JUN-1995; 95WO-US007234.
XX
PR 30-DEC-1994; 94US-00367789.
XX
PA (ASGR-) ASGROW SEED CO.
XX
PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX

DR WPI: 1996-333993/33.
DR P-PSDB; AAR98895.
XX
XX New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
XX Claim 24; Fig 3; 80pp; English.
XX
CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC squash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 771 BP; 176 A; 199 C; 183 G; 213 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4.67e-05 Length: 771
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-857-841-4 (1-14) x AAT34666 (1-771)
OY 1 MetApLySeRgIuSeRThSeRlAgLyARgAsnARgArg 14
DB 3 ATGGACAAATCTGAATCAACGAGTGTGCTGTAACCGTCA 44
RESULT 3
AAT34664
ID AAT34664 standard; DNA; 772 BP.
AC
XX AAT34664;
XX
DT 16-OCT-2003 (revised)
DT 02-DEC-1996 (first entry)
XX
DE Coat protein of the V27 strain of cucumber mosaic virus.
XX
KW Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KW resistance; ss.
XX
OS Cucumber mosaic virus; strain V27.
XX
FH Key Location/Qualifiers
FT CDS 3..659
FT /*tag= a
XX
XX MO9621018-A1.
XX
PD 11-JUL-1996.
XX
PF 07-JUN-1995; 95WO-US007234.
XX
PR 30-DEC-1994; 94US-00367789.
XX
PA (ASGR-) ASGROW SEED CO.
XX
PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;
XX
XX WPI: 1996-333993/33.
DR P-PSDB; AAR98893.
XX
XX New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.
XX
XX Claim 2; Fig 1; 80pp; English.
XX

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 772 BP; 177 A; 202 C; 182 G; 211 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 4.68e-05 | Length: | 772 |
| Score: | 14.00 | Matches: | 14 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-09-857-841-4 (1-14) x AAT34664 (1-772)

OY 1 MetApIySserGjuseThrSerAlaGlyArgAsnArgArg 14
AT17259
Db 3 ATGGACAAATCTGAATCAACAGTGTGCTGAACCGTCGG 44

RESULT 4

ID AAT17259 standard; DNA; 772 BP.

AC AAT17259;

DT 16-OCT-2003 (revised)

DT 02-DEC-1996 (first entry)

DB Coat protein of the A35 strain of cucumber mosaic virus.

KM Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance; ss.

OS Cucumber mosaic virus; strain A35.

FH Key Location/Qualifiers

FT CDS 3..659

FT /*tag= a

PN M09621018-A1.

PD 11-JUL-1996.

PF 07-JUN-1995; 95MO-US007234.

PR 30-DEC-1994; 94US-00367789.

PA (ASGR-) ASGROW SEED CO.

PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

DR MPI: 1996-333993/33.

DR P-PSDB; AAR93803.

XX New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.

XX Disclosure; Fig 8; 80pp; English.

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 772 BP; 175 A; 201 C; 185 G; 211 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 4.68e-05 | Length: | 772 |
| Score: | 14.00 | Matches: | 14 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-09-857-841-4 (1-14) x AAT17259 (1-772)

OY 1 MetApIySserGjuseThrSerAlaGlyArgAsnArgArg 14
AT34665
Db 3 ATGGACAAATCTGAATCAACAGTGTGCTGAACCGTCGG 44

RESULT 5

ID AAT34665 standard; DNA; 773 BP.

AC AAT34665;

DT 16-OCT-2003 (revised)

DT 02-DEC-1996 (first entry)

DB Coat protein of the V33 strain of cucumber mosaic virus.

KM Coat protein; CP; cucumber mosaic virus; CMV; V27; V33; V34; A35;
KM resistance; ss.

OS Cucumber mosaic virus; strain V33.

FH Key Location/Qualifiers

FT CDS 3..659

FT /*tag= a

PN M09621018-A1.

PD 11-JUL-1996.

PF 07-JUN-1995; 95MO-US007234.

PR 30-DEC-1994; 94US-00367789.

PA (ASGR-) ASGROW SEED CO.

PI Boeshore ML, McMaster JR, Tricoli DM, Reynolds JF, Carney KJ;

DR MPI: 1996-333993/33.

DR P-PSDB; AAR98894.

XX New isolated cucumber mosaic virus coat protein DNA - used to produce
PT plants, partic. of the family Cucurbitaceae or Solanaceae, which are
PT resistant to infection.

XX Claim 13; Fig 2; 80pp; English.

CC Coat protein (CP) genes of the V27, V33, V34 and A35 strain of cucumber
CC mosaic virus (CMV) were isolated. The CMV CP genes were isolated from
CC infected plant tissue by PCR amplification of cDNA using primers based on
CC known CP sequences. The genes may be used for producing plants such as
CC quash, cucumber, peppers and tomatoes which are resistant to CMV
CC infection. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 773 BP; 175 A; 200 C; 185 G; 213 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 4.68e-05 | Length: | 773 |
| Score: | 14.00 | Matches: | 14 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-09-857-841-4 (1-14) x AAT34665 (1-773)

```
Oy 1 MetApIySergIuSerThrSerAlaGlyArgAsnArg 14
Db 3 ATGACAAATCTGATCAACCAAGTCTGTCGTAAACCTCGA 44

RESULT 6
AAQ10461
ID AAQ10461 standard; cDNA; 976 BP.
AC AAQ10461;
XX
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 16-APR-1991 (first entry)
DE Capsid protein gene of Cucurbit Mosaic Virus strain FNY.
XX
XX CMV; resistance; capsid protein; Cucumis melo; ss.
XX
XX Cucurbit mosaic virus.
XX
XX Key Location/Qualifiers
XX CDS /*tag= a
/*tag= a
/*product= "CMV strain FNY capsid protein"
XX
XX EP412912-A.
XX
XX 13-FEB-1991.
XX
XX 09-AUG-1990; 90EP-00402282.
XX
XX 11-AUG-1989; 89FR-00010848.
XX
XX (BIOC-) BIOCEM SA.
XX
XX Deboth M, Bentahar S, Noel M, Perret J;
XX
XX WPI; 1991-046027/07.
XX
XX P-PSDB; AARI0652.
XX
XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
XX PT culture on specific medium for new transformed plants etc., esp.
XX PT resistant to cucumber mosaic virus.
XX
XX Claim 15; Page 17; 44pp; French.
XX
XX The gene was isolated from a plasmid (pUC18) containing DNA complementary
XX to RNA 3 of the virulent strain FNY, isolated in New York on infected
XX melons. The sequence includes a leader sequence, coding region and 3' non
XX coding region. The leader sequence is the same length as that of the
XX Japanese Y strain of CMV. Transgenic melon plantlets containing the
XX sequence introduced via an Agrobacterium tumefaciens intermediate are
XX cultured as shoots in special media. The transformed melon plants are
XX resistant to CMV. See also AAQ10462. (Updated on 25-MAR-2003 to correct
XX PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-
XX AUG-2003 to correct OS field.)
XX
XX Sequence 976 BP; 224 A; 249 C; 230 G; 273 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.75e-05 Length: 976
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ10461 (1-976)
Oy 1 MetApIySergIuSerThrSerAlaGlyArgAsnArg 14
Db 75 ATGACAAATCTGATCAACCAAGTCTGTCGTAAACCTCGA 116
```

```
RESULT 7
AAQ10462
ID AAQ10462 standard; DNA; 1007 BP.
XX
XX AAQ10462;
XX
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 16-APR-1991 (first entry)
DE Capsid protein gene of Cucurbit Mosaic Virus strain 117F.
XX
XX CMV; resistance; capsid protein; Cucumis melo; ss.
XX
XX Cucurbit mosaic virus.
XX
XX Key Location/Qualifiers
XX CDS /*tag= a
/*tag= a
/*product= "CMV strain 117F capsid protein"
XX
XX EP412912-A.
XX
XX 13-FEB-1991.
XX
XX 09-AUG-1990; 90EP-00402282.
XX
XX 11-AUG-1989; 89FR-00010848.
XX
XX (BIOC-) BIOCEM SA.
XX
XX Deboth M, Bentahar S, Noel M, Perret J;
XX
XX WPI; 1991-046027/07.
XX
XX P-PSDB; AARI0653.
XX
XX Transgenic melon plantlets prodn. from transformed shoots - by two-stage
XX PT culture on specific medium for new transformed plants etc., esp.
XX PT resistant to cucumber mosaic virus.
XX
XX Claim 16; Page 19; 44pp; French.
XX
XX The gene was isolated from the virulent French strain 117F of CMV. Tomato
XX plantlets at the 2-leaf stage were infected with CMV strain 117F. 15 days
XX post-infection, the virus was purified from the infected leaves and cDNA
XX was synthesised from RNAs 1,2,3 and 4. After purification and selection
XX by standard techniques, cDNA complementary to RNA 4 was found to encode
XX the capsid protein. It was re-cloned into "Blue scribe" plasmids and
XX sequenced. Transgenic melon plantlets containing the sequence introduced
XX via an Agrobacterium tumefaciens intermediate are cultured as shoots in
XX special media. The transformed melon plants are resistant to CMV. See
XX also AAQ10461. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
XX 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
XX field.)
XX
XX Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.91e-05 Length: 1007
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x AAQ10462 (1-1007)
Oy 1 MetApIySergIuSerThrSerAlaGlyArgAsnArg 14
Db 54 ATGACAAATCTGATCAACCAAGTCTGTCGTAAACCTCGA 95

RESULT 8
```



```

AA067395
ID AA067395 standard; DNA; 1007 BP.
XX
AC AA067395;
XX
DT 25-MAR-2003 (revised)
DT 12-APR-1995 (first entry)
XX
DE Cauliflower mosaic virus capsid protein coding sequence.
XX
KM Cauliflower mosaic virus; CMV; capsid protein; coat protein;
XX polyribosyme; inactivate; inactivation; resistance; crop protection; ss.
XX
OS Cauliflower mosaic virus.
XX
FH Key Location/Qualifiers
FT CDS 54..710
FT /*tag= a
FT /product= "Capsid protein."
XX
PN FR2701960-A1.
XX
PD 02-SEP-1994.
XX
PF 26-FEB-1993; 93FR-00002269.
XX
PR 26-FEB-1993; 93FR-00002269.
XX
PA (GENE-) GENE SHEARS PTY LTD.
XX
PI Lenee P, Perez P, Gruber V, Baudot G, Ollivo C;
XX
DR WPI; 1994-281767/35.
DR P-PSDB; AAR57968.
XX
PT New polyribosyme contg. several catalytic regions in complementary
PT sequence - can inactivate gene for viral capsid protein, esp. for prepn.
PT of new virus resistant transgenic plants, also DNA sequence encoding it.
XX
PS Disclosure; Fig 2; 67pp; French.
XX
CC The RNA encoding the capsid protein of cauliflower mosaic virus can be
CC targeted by a nucleic acid sequence called a "polyribosyme". The
CC polyribosyme has endoribonuclease activity and is able to inactivate the
CC gene encoding the viral capsid protein. The polyribosyme comprises
CC several catalytic regions derived from ribozymes and confers complete
CC resistance to virus. See AA067391-94. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 1007 BP; 227 A; 259 C; 247 G; 274 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 5.91e-05 Length: 1007
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
XX
US-09-857-841-4 (1-14) x AA067395 (1-1007)
OY 1 MetApLySserGluSerThrSerAlaGlyArgAsnArg 14
Db 54 ATGGACAAATCTGAATCAACAGTCTGTCGTAAACCGTCA 95
RESULT 9
AAT99545/c
ID AAT99545 standard; cDNA; 1066 BP.
XX
AC AAT99545;
XX
DT 25-MAR-2003 (revised)
DT 21-MAY-1998 (first entry)

```

```

XX
DE Cucumber mosaic virus RNA-3 cDNA fragment.
XX
KM Transgenic plant; virus resistance; disease resistance; RNA virus; CMV;
XX coat protein; antisense gene; ss.
XX
OS Cucumber mosaic virus.
XX
FH Key Location/Qualifiers
FT 3'UTR 1..299
FT /*tag= a
FT CDS 300..958
FT /*tag= b
FT /product= "coat protein"
FT sig_peptide 956..1029
FT /*tag= c
FT /note= "coat protein leader sequence"
FT promoter 1030..1066
FT /*tag= d
FT /note= "F sequence of sub-genomic promoter"
XX
PN EP806481-A2.
XX
PD 12-NOV-1997.
XX
PF 07-MAY-1997; 97EP-00201379.
XX
PR 09-MAY-1996; 96IT-MI000927.
XX
PA (META-) METAPONTUM AGROBIOS SCRL.
XX
PI Cellini F, Grieco PD;
XX
DR WPI; 1997-538620/50.
XX
PT Preparing transgenic plants resistant to RNA virus infection - using
PT anti-sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
PS Claim 3; Page 10; 18pp; English.
XX
CC This cDNA clone of cucumber mosaic virus (CMV) RNA-3 includes domain P of
CC the subgenomic promoter of viral RNA, the coat protein gene, its leader
CC sequence, and the RNA-like 3'-terminal region of RNA-3. It was prepared
CC by amplifying a fragment of CMV cDNA-3 from clone PCR-CMV1RNA3 by PCR
CC (see also AAT99548-49). The gene construct is introduced into a vector
CC containing a promoter active in plant cells in antisense orientation
CC relative to the promoter. A claimed recombinant vector comprises the
CC plant promoter, the antisense gene construct and a terminator which is
CC functional in the plant. In addition to CMV, viral RNA may also be used
CC from tobacco mosaic virus and potato virus. Claimed transgenic plants
CC have the antisense gene construct integrated into their genomes. They are
CC resistant to viral infection. In particular, they are resistant to CMV.
CC Within the antisense gene construct, the interfering activity of the
CC antisense P domain of the sub-genomic promoter, associated with the
CC antisense activity performed by the coat protein gene, allows production
CC of plants having 100% resistance to CMV. (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 1066 BP; 299 A; 251 C; 273 G; 243 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 6.22e-05 Length: 1066
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
XX
US-09-857-841-4 (1-14) x AAT99545 (1-1066)
OY 1 MetApLySserGluSerThrSerAlaGlyArgAsnArg 14

```

DB 956 ATGACAAATCTGAATCAACGAGTGTGCTGAACCTCGA 915
RESULT 10
AAZ07505/c
ID AAZ07505 standard; cDNA, 1067 BP.
XX
AC AAZ07505;
XX
DT 26-NOV-1999 (first entry)
XX
DE Cucumber mosaic virus (CMV) RNA-3 gene cDNA clone fragment.
XX
KM Transgenic plant; RNA virus; antisense construct; cucumber mosaic virus;
KM CMV; promoter; coat protein gene; infection; RNA-3; 89.
XX
OS Cucumber mosaic virus.
XX
PN US5959181-A.
XX
PD 28-SEP-1999.
XX
PF 09-MAY-1997; 97US-00854170.
XX
PR 09-MAY-1996; 96IT-MI000927.
XX
PA (META-) METAPONTUM AGROBIOS SCRL.
XX
PI Cellini F, Grieco PD;
XX
DR WPI; 1997-538620/50.
XX
PT Preparing transgenic plants resistant to RNA virus infection - using
PT anti-sense gene constructs containing the viral coat protein gene, e.g.
PT from cucumber mosaic virus.
XX
PS Claim 2; Fig 1; 15pp; English.
XX
CC The invention relates to preparing transgenic plants resistant to RNA
CC virus induced infections that comprises integrating an antisense gene
CC construct into the plant genome. The construct comprises: (a) an F domain
CC of a subgenomic promoter of cucumber mosaic virus (CMV); (b) downstream
CC from the subgenomic promoter, a leader sequence of a coat protein gene of
CC CMV; (c) downstream from the leader sequence, a 3'-terminal region of a CMV
CC coat protein gene. The method is useful for producing plants which are
CC resistant to infection by RNA based viruses. The gene construct gives
CC higher levels of resistance compared to antisense constructs which are
CC capable of complementing with different domains of genomic RNA of CMV.
CC The present sequence represents the fragment of cDNA clone of RNA-3 of
CC CMV. This forms the antisense construct of the invention
XX
SQ Sequence 1067 BP; 297 A; 250 C; 276 G; 244 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 6.22e-05 Length: 1067
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-857-841-4 (1-14) x AAZ07505 (1-1067)
OY 1 MetAplysSergIuSerThSeraIaGlyARgAsnARgArg 14
ID AAAN81111 standard; DNA, 1379 BP.
XX
AC AAAN81111;
XX
XX
RESULT 11
ID AAAN81111 standard; DNA, 1379 BP.
XX
AC AAAN81111;
XX
XX

DT 25-MAR-2003 (revised)
DT 12-NOV-1990 (first entry)
XX
DE Sequence contg. CMV strain Y coat protein gene.
XX
KM Cucumber mosaic virus; plant viral resistance; 88.
XX
XX Synthetic.
XX
OS
XX
FT Key Location/Qualifiers
FT CDS 418..1074
FT /*tag= a
FT /label= cucumber mosaic virus-Y coat protein.
XX
PN EP279433-A.
XX
PD 24-AUG-1988.
XX
PF 18-FEB-1988; 88EP-00102322.
XX
PR 20-FEB-1987; 87JP-00038288.
PR 25-FEB-1987; 87JP-00043443.
PR 18-FEB-1988; 88JP-00035809.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Furusawa I, Onda H, Komiya T;
XX
DR WPI; 1988-236708/34.
XX
P-PSDB; AAP80509.
XX
PT DNA coding for the coat protein of cucumber mosaic virus strain Y - used
PT for producing plants resistant to cucumber mosaic virus infection.
XX
PS Disclosure; Page ?; 20pp; English.
XX
CC This DNA is produced on screening of a plasmid library and is used to
CC transform plant cells which subsequently produce the coat prot- ein of
CC cucumber mosaic virus (CMV) strain Y. This protein is not synthesised in
CC natural plant cells. The resistance to CMV infect- ion, provided by the
CC DNA, is shown in plant cells and redifferent- iated plant bodies. See
CC also AAAN81110. (updated on 25-MAR-2003 to correct PR field.) (updated on
CC 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1379 BP; 306 A; 342 C; 333 G; 398 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 7.81e-05 Length: 1379
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-09-857-841-4 (1-14) x AAAN81111 (1-1379)
OY 1 MetAplysSergIuSerThSeraIaGlyARgAsnARgArg 14
ID AAQ76107 standard; DNA, 1696 BP.
XX
AC AAQ76107;
XX
DT 25-MAR-2003 (revised)
DT 20-JUL-1995 (first entry)
XX
DE Cucumber mosaic virus RNA-3 chimera encoding RNase TI.
XX
KM Cucumber mosaic virus; tomato mosaic virus; minus-strand RNA;
KM virus resistance; disease resistance; transgenic plant; cross protection;
KM


```

XX OS Cucurbit mosaic virus.
XX FH Key Location/Qualifiers
XX CDS 123..914
FT /*tag= a
FT /product= "Tomv P30 elicitor"
XX
XX MO9429464-A1.
XX
XX PD 22-DEC-1994.
XX PF 03-JUN-1994; 94WO-EP001817.
XX PR 04-JUN-1993; 93GB-00011593.
XX
XX PA (SANO ) SANDOZ LTD.
XX PA (SANO ) SANDOZ PATENT GMBH.
XX PA (SANO ) SANDOZ-ERFINDUNGEN VERN GES MBH.
XX PI De Haan PT;
XX WPI; 1995-036490/05.
XX P-PSDB; AAR67755.
XX
XX PT DNA constructs for imparting pathogen, esp. virus, resistance to plants -
XX PT encodes RNA that interacts with viral RNA polymerase to generate an
XX PT eliciting agent.
XX
XX PS Claim 5; Page 34-35; 50pp; English.
XX
XX CC A chimeric cucumber mosaic virus RNA-3 (given in AAQ76108) has the coat
XX CC protein gene replaced by a gene encoding an elicitor, Tomv P30, having
XX CC the sequence given in AAR67755. The construct elicits a minus-sense RNA
XX CC that interacts with the RNA-dependent RNA-polymerase of an invading
XX CC virus, thus conferring virus-resistance on a host plant, e.g. tobacco,
XX CC tomato. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 2173 BP; 561 A; 438 C; 532 G; 642 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0.000117 Length: 2173
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
XX
US-09-857-841-4 (1-14) x AAQ76108 (1-2173)
OY 1 MetApLySserGluSerThrSerAlaGlyArgAsnArg 14
DB 1210 ATGGACAATCTGATCAACCAAGTGTGCTGTAACGTCGA 1251
XX
RESULT 15
XX ID AAQ03641 standard; DNA; 657 BP.
XX AC AAQ03641;
XX
XX DT 24-OCT-2003 (revised)
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 07-AUG-1990 (first entry)
XX
XX DE Cucumber Mosaic Virus-C (CMV-C) coat protein gene.
XX
XX KW CMV-C; cucurbitaceae; solanaceae; ds.
XX
XX OS Cucumber mosaic virus; strain C.
XX
XX PM MO9002185-A.
XX

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```

PD 08-MAR-1990.
XX
XX PF 02-AUG-1989; 89WO-US003288.
XX
XX PR 19-AUG-1988; 88US-00234404.
XX
XX PA (UPJO ) UPJOHN CO.
XX PA (CORR ) CORNELL RES FOUND INC.
XX
XX PI Quemada H, Slightom UL, Gonsalves D, Kearney C;
XX
XX WPI; 1990-099409/13.
XX
XX PT Coat protein gene of cucumber mosaic virus strain WL - cloned to produce
XX PT transformed plants which are resistant to CMV viral infection.
XX
XX PS Disclosure; Page ?; 18pp; English.
XX
XX CC The sequence encodes the coat protein of CMV-C. (Updated on 25-MAR-2003
XX CC to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)
XX CC (Updated on 27-AUG-2003 to correct OS field.) (Updated on 24-OCT-2003 to
XX CC standardise OS field)
XX
XX SQ Sequence 657 BP; 157 A; 176 C; 151 G; 173 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0.00396 Length: 657
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.71% Indels: 0
DB: 2 Gaps: 0
XX
US-09-857-841-4 (1-14) x AAQ03641 (1-657)
OY 1 MetApLySserGluSerThrSerAlaGlyArgAsn 12
DB 1 ATGGACAATCTGATCAACCAAGTGTGCTGTAAC 36
XX

```

Search completed: December 5, 2004, 09:53:57
Job time : 328 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus2n model

Run on: December 5, 2004, 09:41:23 ; Search time 2043 Seconds

(without alignments)
249.709 Million cell updates/sec

Title: US-09-857-841-4
Sequence: 1 MDKSESTAGNR 14

Scoring table:
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Word size: 1

Total number of hits satisfying chosen parameters: 65640016

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE=frame+g2n.model -DEV=xln
-Q=/cgm2_1/USPTO.epool/US09857841/runat_03122004_160613_19127/app_query.fasta_1.199
-DB=EST -QFMT=fastcap -SUFFIX=olip2n.rst -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALL=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=plc
-NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09857841.qcgm2_1.13437@runat_03122004_160613_19127 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6
-Fgapext=7 -Ygapop=60 -Ygapext=60 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_g881: *
9: gb_g882: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|-------|--------------------|
| C 1 | 14 | 100.0 | 127 4 | BM067231 KS08001E1 |
| C 2 | 9 | 64.3 | 801 8 | BZ560224 |
| C 3 | 8 | 64.3 | 957 8 | BZ560224 msh2.164 |
| C 4 | 8 | 57.1 | 172 2 | B8571483 |
| C 5 | 8 | 57.1 | 297 2 | B8571483 msh2.191 |
| C 6 | 8 | 57.1 | 402 1 | AA560203 |
| C 7 | 8 | 57.1 | 536 9 | AA560203 v120h03.r |
| C 8 | 8 | 57.1 | 589 9 | AA560203 HS_5107_B |
| C 9 | 8 | 57.1 | 594 7 | CF568826 tigr-g85 |
| | | | | CF568862 FAMU_USDA |

| | | | | | |
|------|---|------|--------|----------|----------|
| C 10 | 8 | 57.1 | 679 8 | A2419370 | A2419370 |
| C 11 | 8 | 57.1 | 686 8 | A2964281 | A2964281 |
| C 12 | 8 | 57.1 | 816 8 | A2741218 | A2741218 |
| C 13 | 8 | 57.1 | 823 4 | B1851822 | B1851822 |
| C 14 | 8 | 57.1 | 839 8 | B2603235 | B2603235 |
| C 15 | 8 | 57.1 | 889 9 | C6137878 | C6137878 |
| C 16 | 8 | 57.1 | 899 9 | CG225585 | CG225585 |
| C 17 | 8 | 57.1 | 900 9 | CG623795 | CG623795 |
| C 18 | 8 | 57.1 | 908 9 | CG623807 | CG623807 |
| C 19 | 8 | 57.1 | 939 2 | BB895594 | BB895594 |
| C 20 | 8 | 57.1 | 953 5 | BU112365 | BU112365 |
| C 21 | 8 | 57.1 | 964 9 | CG368624 | CG368624 |
| C 22 | 8 | 57.1 | 1015 5 | BU147745 | BU147745 |
| C 23 | 8 | 57.1 | 1345 8 | CC312068 | CC312068 |
| C 24 | 8 | 57.1 | 1678 8 | CC222612 | CC222612 |
| C 25 | 8 | 57.1 | 1907 2 | BF144190 | BF144190 |
| C 26 | 7 | 50.0 | 109 1 | AA784543 | AA784543 |
| C 27 | 7 | 50.0 | 118 6 | CD945181 | CD945181 |
| C 28 | 7 | 50.0 | 118 6 | CD960094 | CD960094 |
| C 29 | 7 | 50.0 | 129 8 | CC387216 | CC387216 |
| C 30 | 7 | 50.0 | 136 8 | BH804848 | BH804848 |
| C 31 | 7 | 50.0 | 145 6 | CF096437 | CF096437 |
| C 32 | 7 | 50.0 | 148 8 | A2481650 | A2481650 |
| C 33 | 7 | 50.0 | 156 7 | CO744011 | CO744011 |
| C 34 | 7 | 50.0 | 162 9 | CG541742 | CG541742 |
| C 35 | 7 | 50.0 | 177 2 | AW859218 | AW859218 |
| C 36 | 7 | 50.0 | 193 2 | AW859260 | AW859260 |
| C 37 | 7 | 50.0 | 201 8 | CC114971 | CC114971 |
| C 38 | 7 | 50.0 | 207 1 | AV264210 | AV264210 |
| C 39 | 7 | 50.0 | 215 9 | CG481915 | CG481915 |
| C 40 | 7 | 50.0 | 219 9 | CG483642 | CG483642 |
| C 41 | 7 | 50.0 | 224 2 | AW210914 | AW210914 |
| C 42 | 7 | 50.0 | 234 1 | A1212359 | A1212359 |
| C 43 | 7 | 50.0 | 234 9 | CG490292 | CG490292 |
| C 44 | 7 | 50.0 | 235 9 | CG632317 | CG632317 |
| C 45 | 7 | 50.0 | 240 7 | F25547 | F25547 |

ALIGNMENTS

RESULT 1
BM067231/c 127 bp mRNA linear EST 11-SEP-2002
KS08001E12 KS08 Capsicum annuum cDNA, mRNA sequence.

BM067231.1 GI:22787366

LOCUS
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

EST.
Capsicum annuum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Capsicum.

REFERENCE
1 (bases 1 to 127)
Lee, S., Kim, S.-Y., Chung, Y.-H., Shin, H.-J., Goh, S.-H., Pai, H.-S., Hur, C.-G. and Choi, D.

Generation of Expressed Sequence Tags from Hot Pepper (Capsicum annuum L.) and Sequence Analysis in Relation to Hypersensitive Response Against Pathogen

Unpublished (2001)

JOURNAL
COMMENT

Genome Research Center and National Center for Genome Information
Korea Research Institute of Bioscience and Biotechnology
P.O. Box 115, Yuseong, Taejeon, 305-600, Republic of Korea

Tel: 82-42-860-4309
Fax: 82-42-860-4309

Email: doil@mail.kribb.re.kr

High quality sequence stop: 127.

FEATURES
source

Location/Qualifiers
1..127
/organism="Capsicum annuum"
/mol_type="mRNA"
/cultiivar="Hang Keun"
/db_xref="taxon:4072"

ORIGIN

/tissue_type="anther"
/dev_stage="10 weeks after germination"
/clone_lib="KS08"
/note="Vector: pBluescript SK(-)"

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 7.61e-05 | Length: | 127 |
| Score: | 14.00 | Matches: | 14 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-09-857-841-4 (1-14) x BM067231 (1-127)

OY 1 MetaplyserGluserThSeraIaGlyArgAnaRg 14
|||||
78 ATGACAAATCTGAATCAACAGTGTGCTGTAACCGTCA 37

RESULT 2
LOCUS BZ560224 801 bp DNA linear GSS 17-DEC-2002
DEFINITION pac82-164_2261.xl pac82-164 Pseudomonas aeruginosa genomic clone

ACCESSION BZ560224
VERSION BZ560224.1 GI:27177889
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 801)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V. Whole-Genome-Sequence Variation among multiple isolates of
Pseudomonas aeruginosa library

JOURNAL J. Bacteriol. (2002) In press
CONTACT: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

FEATURES

source Location/Qualifiers
1..801
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
/clone="pac82-164_2261"
/clone_lib="pac82-164"
/note="Clinical isolate 2-164 whole genomic shotgun
library."

ORIGIN

Alignment Scores:

| | | | |
|------------------------|---------|---------------|-----|
| Pred. No.: | 37 | Length: | 801 |
| Score: | 9.00 | Matches: | 9 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 64.29% | Indels: | 0 |
| DB: | 8 | Gaps: | 0 |

US-09-857-841-4 (1-14) x BZ560224 (1-801)

OY 6 SerThSeraIaGlyArgAnaRg 14
|||||
Db 458 AGTACATCGCGCGGTAGAAACCGCGCT 432

RESULT 3

BZ571483/c BZ571483 957 bp DNA linear GSS 17-DEC-2002
LOCUS meh2_191.y1 msh Pseudomonas aeruginosa genomic clone meh2_191,
genomic survey sequence.

ACCESSION BZ571483
VERSION BZ571483.1 GI:27206544
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 957)
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V. Whole-Genome-Sequence Variation among multiple isolates of
Pseudomonas aeruginosa library

JOURNAL J. Bacteriol. (2002) In press
CONTACT: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

FEATURES
source Location/Qualifiers
1..957
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="msh"
/db_xref="taxon:287"
/clone="meh2_191"
/clone_lib="msh"
/note="Environmental isolate. Whole genomic shotgun
library."

ORIGIN

Alignment Scores:

| | | | |
|------------------------|---------|---------------|-----|
| Pred. No.: | 43.5 | Length: | 957 |
| Score: | 9.00 | Matches: | 9 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 64.29% | Indels: | 0 |
| DB: | 8 | Gaps: | 0 |

US-09-857-841-4 (1-14) x BZ571483 (1-957)

OY 6 SerThSeraIaGlyArgAnaRg 14
|||||
Db 422 AGTACATCGCGCGGTAGAAACCGCGCT 396

RESULT 4
LOCUS BBS74268 172 bp mRNA linear EST 30-NOV-2000
DEFINITION BBS74268 RIKEN full-length enriched, 11 days pregnant adult female
ovary and uterus Mus musculus CDNA clone 5033401A11, mRNA sequence.

ACCESSION BBS74268
VERSION BBS74268.1 GI:11470812
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T.,
Carninci,P., Hanagaki,T., Hayatsu,N., Hirose,T., Hirozane,T.,
Hodoyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J.,
Kojima,Y., Kono,H., Kusakabe,M., Matsuyama,T., Miyazaki,A.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y.,
Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K.,
Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Sogabe,Y.,
Suzuki,H., Tagawa,A., Takehashi,F., Tanaka,T., Toya,T.,
Watanishi,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A.,

REFERENCE
1 (bases 1 to 402)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus

AUTHORS
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Thibaut, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMNI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MG1:553549
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 387.
Location/Qualifiers
1. .402
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:972821"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse tcell 937311"
/note="Organ: blood; Vector: pluescript SK-; Site: 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector: ~5' adaptor sequence: 5' GAATTCGACGACGAG
3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

ORIGIN

Alignment Scores:

| Pred. No.: | 193 | Length: | 402 |
|------------------------|---------|---------------|-----|
| Score: | 8.00 | Matches: | 8 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 57.14% | Indels: | 0 |
| DB: | 1 | Gaps: | 0 |

US-09-857-841-4 (1-14) x AA560203 (1-402)

CY 7 ThrsrAlaGlyArgAsnArgArg 14
|||||
DB 269 ACCTCTGACGACGAGATCTGAGA 292
|||||

RESULT 7
A0612674/c
LOCUS A0612674 536 bp DNA linear GSS 15-JUN-1999
DEFINITION H5_5107_B2_E12_T7A RPCT-11 Human Male BAC library Homo sapiens
genomic clone Plate=683 Col=24 Row=J, genomic survey sequence.
ACCESSION A0612674
VERSION A0612674
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 536)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (117), 9739-9744 (1999)
JOURNAL MEDLINE 99380589
PUBMED 10449784
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center

University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCT-11. For BAC
library availability, please contact Pieter de Jong
pieter@ejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering/bac.htm)
or from Research Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 683 Row: J Column: 24
Seq primer: T7
Class: BAC ends
High quality sequence stop: 536.
Location/Qualifiers
1. .536
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=683 Col=24 Row=J"
/sex="male"
/clone_lib="RPCT-11 Human Male BAC library"
/note="Vector: pBAC3.6; Site: 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"

ORIGIN

Alignment Scores:

| Pred. No.: | 251 | Length: | 536 |
|------------------------|---------|---------------|-----|
| Score: | 8.00 | Matches: | 8 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 57.14% | Indels: | 0 |
| DB: | 8 | Gaps: | 0 |

US-09-857-841-4 (1-14) x A0612674 (1-536)

CY 5 GluSerThrSerAlaGlyArgAsn 12
|||||
DB 486 GAGAGCACATCTGCCGCCGCAAT 463
|||||

RESULT 8
CE588296/c
LOCUS CE588296 589 bp DNA linear GSS 28-SEP-2003
DEFINITION c1gr-gss-dog-17000366361600 Dog library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE588296
VERSION CE588296
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 589)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
TITLE The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
JOURNAL MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun.
Location/Qualifiers

source
1..589
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN
Alignment Scores:
Pred. No.: 273 Length: 589
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 9 Gaps: 0

US-09-857-841-4 (1-14) x CFS68862 (1-589)

Oy 5 GUSerThSerAlaGlyArgAsn 12
|||||
516 GAGTCAACCACTGCTCGAAGAACA 493

RESULT 9
LOCUS CFS68862 594 bp mRNA linear EST 23-SEP-2003
DEFINITION FAMU_USDA_FP_00084 Vitis shuttleworthii L., grape Vitis
shuttleworthii cDNA 5', mRNA sequence.
CF568862
ACCESSION CFS68862
VERSION CFS68862.1 GI:34994945
KEYWORDS EST.
SOURCE Vitis shuttleworthii
ORGANISM Vitis shuttleworthii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 594)
REFERENCE Hunter,W.B., Dang,P.M., Chaparro,J.X., Lu,J. and Leong,S.
Genes expressed in Vitis shuttleworthii L
JOURNAL Unpublished (2004)
COMMENT Contact: Jiang Lu, FAMU, Wayne Hunter, USDA,ARS
Viticulture Centre, FAMU, Tallahassee, FL
Tallahassee, FL 32317, USA
Tel: (850) 412-7393
Fax: (850) 561-2617, (772) 462-5898
Email: jiang.lu@fam.u.edu,
Seq primer: T3 Primer.
FEATURES
Location/Qualifiers
1..594
/organism="Vitis shuttleworthii"
/mol_type="mRNA"
/db_xref="taxon:246827"
/sex="Mixed population"
/tissue_type="Entire tendril, leaves, bud, flowers"
/dev_stage="At blooming"
/lab_host="XLI-Blue"
/clone_lib="Vitis shuttleworthii L., grape"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; A high quality EST with at least 100 contiguous
bases at Trace Tuner score of 20 or better. Construction
by FW Dang, USDA, ARS, U.S. Horticultural Research Lab,
Ft. Pierce, FL, USA."

ORIGIN
Alignment Scores:
Pred. No.: 275 Length: 594
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 7 Gaps: 0

US-09-857-841-4 (1-14) x CFS68862 (1-594)

Oy 7 ThSerAlaGlyArgAsnArgArg 14
|||||
82 ACATCTCAGGAGGAGAAATCGAGA 105

RESULT 10
LOCUS AZ419370/c 679 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0195P18R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG1M0195P18 R, genomic survey sequence.
AZ419370
ACCESSION AZ419370
VERSION AZ419370.1 GI:10543383
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 679)
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0195 row: P column: 18
Seq primer: CACACAGAAACAGCTATGAC
Class: plasmid end
High quality sequence stop: 679.
FEATURES
Location/Qualifiers
1..679
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0195P18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[gB]AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E.coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.: 311 Length: 679

Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservatave: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 57.14% Indels: 0
 DB: 8 Gaps: 0

US-09-857-841-4 (1-14) x AZ419370 (1-679)

Qy 7 ThrsEralagiYArGAsnArGArg 14
 63 ACCTCTGCAGCAGCAATCTGTA 40

RESULT 11

AZ964281/c 686 bp DNA linear GSS 27-APR-2001
 LOCUS 2M0233J19R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 DEFINITION clone UUGC2M0233J19 R, genomic survey sequence.

ACCESSION AZ964281
 VERSION AZ964281.1 GI:13835508
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 686)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0233 row: J column: 19
 Seg primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 686.
 Location/Qualifiers

FEATURES

source

1. 686
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="UUGC2M0233J19"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: pMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g14732114[gb]|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 Chemically-competent E. coli XL10-Gold (Stratagene) cells

ORIGIN and selected for ampicillin resistance."

Alignment Scores:

Pred. No.: 314 Length: 686
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservatave: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 57.14% Indels: 0
 DB: 8 Gaps: 0

US-09-857-841-4 (1-14) x AZ964281 (1-686)

Qy 6 SerThrsEralagiYArGAsnArGArg 13
 163 TCTACATCAGCAGCAGCAATAATAGA 140

RESULT 12

AZ741218/c 816 bp DNA linear GSS 25-JAN-2001
 LOCUS RPCI-24-145M10.TJ RPCI-24 Mus musculus genomic clone
 DEFINITION RPCI-24-145M10, genomic survey sequence.

ACCESSION AZ741218
 VERSION AZ741218.1 GI:12515463
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 816)
 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levine, M.,
 Tesegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,
 Russell, D., de Jong, P. and Fraser, C.M.
 Mouse BAC End Sequences from Library RPCI-24
 Unpublished (1999)

TITLE Other GSSs: RPCI-24-145M10.TV

JOURNAL Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@mail.cho.org). Clones may be purchased from BACPAC
 Resources (http://www.choi.org/bacpac/orderingframe.htm). BAC end
 page: http://www.tigr.org/tcd/bac_ends/mouse/bac_end_intro.html
 Plate: 145 row: M column: 10
 Seg primer: SP6
 Class: BAC ends.
 Location/Qualifiers

FEATURES

source

1. 816
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-24-145M10"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /clone_lib="RPCI-24"
 /note="Vector: pPARBAC1, Site 1: BamHI, Site 2: BamHI;
 RPCI-24 Mouse BAC library produced by Pieter de Jong. The
 library was cloned in the pPARBAC1 cloning vector at the
 BamHI sites using MboI partially digested male C57BL/6J
 DNA."

ORIGIN

Alignment Scores:

Pred. No.: 368 Length: 816
 Score: 8.00 Matches: 8
 Percent Similarity: 100.00% Conservatave: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 57.14% Indels: 0
DB: 8 Gaps: 0
US-09-857-841-4 (1-14) x AZ741218 (1-816)
QY 3 LysSerGluSerThrSerAlaGly 10
487 AAGTCAGGCTCTACTCTGCTGGT 464
RESULT 13
BI851822/c 823 bp mRNA linear EST 10-OCT-2001
LOCUS 603378972F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5391617 5',
DEFINITION mRNA sequence.
ACCESSION BI851822.1 GI:15992569
VERSION BI851822.1 GI:15992569
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 823)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapb-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
Plate: L1AM1197 row: p column: 18
High quality sequence stop: 773.
FEATURES
location/Qualifiers
1..823
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5391617"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_id="NCI CGAP Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Alignment Scores:
Pred. No.: 371 Length: 823
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 4 Gaps: 0
US-09-857-841-4 (1-14) x BI851822 (1-823)
QY 5 GluSerThrSerAlaGlyArgAsn 12
727 GAGAGCACCAAGCGCTCGAAGAAAT 704
RESULT 14
BZ603235 839 bp DNA linear GSS 08-JUN-2003
LOCUS WHADAS5TF Human MCF7 breast cancer cell line library (MCF7_1) Homo
DEFINITION sapiens genomic clone MCF7_1-19021, genomic survey sequence.
ACCESSION BZ603235

VERSION BZ603235.1 GI:31511697
GSS.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 839)
AUTHORS Volik,S., Zhao,S., Chin,K., Brebner,J.H., Herndon,D.R., Tao,Q.,
Kowbel,D., Huang,G., Lapuk,A., Kuo,W.-L., Magrane,G., de Jong,P.,
Gray,J.W. and Collins,C.
End-sequence profiling: Sequence-based analysis of aberrant genomes
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
PUBMED 22709111
MEDLINE 12788976
COMMENT Contact: Volik SV
Colin Collins' lab
USF Comprehensive Cancer Center
USF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.usf.edu
This clone is available from Amplicon Express
<http://www.genomex.com>
Class: BAC ends.
FEATURES
location/Qualifiers
1..839
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="MCF7_1-19021"
/sex="female"
/clone_id="Human MCF7 breast cancer cell line library
(MCF7_1)"
/note="Vector: pCBAC1; Site 1: HindIII; This library was
constructed from MCF7 breast cancer cell line by Amplicon
Express (<http://www.genomex.com>) using their standard
procedure."

ORIGIN
Alignment Scores:
Pred. No.: 378 Length: 839
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 8 Gaps: 0
US-09-857-841-4 (1-14) x BZ603235 (1-839)
QY 4 SerGluSerThrSerAlaGlyArg 11
721 TCAGAAAGCACTTCAGCGGTCG 744
RESULT 15
CG137878/c 889 bp DNA linear GSS 21-AUG-2003
LOCUS PUTCG49TD_ZM_0_6_1.0_XB Zee mays genomic clone ZMBR05050J1,
DEFINITION genomic survey sequence.
ACCESSION CG137878
VERSION CG137878.1 GI:34028661
KEYWORDS GSS.
SOURCE Zee mays
ORGANISM Zee mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zee.
REFERENCE 1 (bases 1 to 889)
AUTHORS Whiteaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Reenick,A., Fraser,C.W., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
COMMENT Other_GSSs: PUTCG49TB

Contact: Cathy WhiteLaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whiteLaw@tigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

FEATURES

source

1..889

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZMMBTA0550J01"

/clone_lib="ZM 0.6-1.0 KB"

/note="Vector: pCR4-TOPO, Site_1: EcoRI, 0.6-1.0 kb high

COT selected genomic DNA library"

ORIGIN

Alignment Scores:

| | | | |
|------------------------|---------|---------------|-----|
| Pred. No.: | 398 | Length: | 889 |
| Score: | 8.00 | Matches: | 8 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 57.14% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-09-857-841-4 (1-14) x CG137878 (1-889)

QY 5 G|USeRThSeR|Ag|YArqAn 12

Db 600 GAATCAACACAGTGTGGAAGGAT 577

Search completed: December 5, 2004, 11:10:41
Job time : 2048 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 09:47:13 ; Search time 68 Seconds
(without alignments)
146.339 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 14
Sequence: 1 MDKSESTSGAGNR 14

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1640630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09857841/runat_03122004_160614_19150/app_query.fasta.1.199
-DB=Issued_Patents_NA -QEMT=fastap -SUFFIX=olip2n.rnl -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09857841.cgn2_1.1_69.qrunat_03122004_160614_19150 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESUBSTR -NEG SCORES=0 -WAIT -DSPLLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 14 | 100.0 | 130 | 1 | US-08-090-193-14 |
| 2 | 14 | 100.0 | 130 | 2 | US-08-488-031-14 |
| 3 | 14 | 100.0 | 130 | 2 | US-08-488-569-14 |
| 4 | 14 | 100.0 | 130 | 2 | US-08-488-027-14 |
| 5 | 14 | 100.0 | 130 | 2 | US-08-090-192-14 |
| 6 | 14 | 100.0 | 130 | 2 | US-08-482-663-14 |
| 7 | 14 | 100.0 | 130 | 3 | US-08-482-658-14 |
| 8 | 14 | 100.0 | 130 | 3 | US-08-470-349-14 |
| 9 | 14 | 100.0 | 130 | 3 | US-08-475-610-14 |
| 10 | 14 | 100.0 | 130 | 5 | PCT-US92-00277-14 |
| 11 | 14 | 100.0 | 130 | 5 | PCT-US92-00278-14 |
| 12 | 14 | 100.0 | 131 | 1 | US-08-090-193-11 |

| | | | | | | |
|----|----|-------|-----|---|-------------------|-------------------|
| 13 | 14 | 100.0 | 131 | 2 | US-08-488-031-11 | Sequence 11, Appl |
| 14 | 14 | 100.0 | 131 | 2 | US-08-486-569-11 | Sequence 11, Appl |
| 15 | 14 | 100.0 | 131 | 2 | US-08-488-027-11 | Sequence 11, Appl |
| 16 | 14 | 100.0 | 131 | 2 | US-08-090-192-11 | Sequence 11, Appl |
| 17 | 14 | 100.0 | 131 | 2 | US-08-482-663-11 | Sequence 11, Appl |
| 18 | 14 | 100.0 | 131 | 3 | US-08-482-658-11 | Sequence 11, Appl |
| 19 | 14 | 100.0 | 131 | 3 | US-08-470-349-11 | Sequence 11, Appl |
| 20 | 14 | 100.0 | 131 | 3 | US-08-475-610-11 | Sequence 11, Appl |
| 21 | 14 | 100.0 | 131 | 5 | PCT-US92-00277-11 | Sequence 11, Appl |
| 22 | 14 | 100.0 | 131 | 5 | PCT-US92-00278-11 | Sequence 11, Appl |
| 23 | 14 | 100.0 | 152 | 1 | US-08-090-193-9 | Sequence 9, Appl |
| 24 | 14 | 100.0 | 152 | 1 | US-08-090-193-10 | Sequence 9, Appl |
| 25 | 14 | 100.0 | 152 | 2 | US-08-488-031-9 | Sequence 9, Appl |
| 26 | 14 | 100.0 | 152 | 2 | US-08-488-031-10 | Sequence 9, Appl |
| 27 | 14 | 100.0 | 152 | 2 | US-08-486-569-9 | Sequence 9, Appl |
| 28 | 14 | 100.0 | 152 | 2 | US-08-486-569-10 | Sequence 9, Appl |
| 29 | 14 | 100.0 | 152 | 2 | US-08-488-027-9 | Sequence 9, Appl |
| 30 | 14 | 100.0 | 152 | 2 | US-08-488-027-10 | Sequence 9, Appl |
| 31 | 14 | 100.0 | 152 | 2 | US-08-090-192-9 | Sequence 9, Appl |
| 32 | 14 | 100.0 | 152 | 2 | US-08-090-192-10 | Sequence 9, Appl |
| 33 | 14 | 100.0 | 152 | 2 | US-08-482-663-9 | Sequence 9, Appl |
| 34 | 14 | 100.0 | 152 | 2 | US-08-482-663-10 | Sequence 9, Appl |
| 35 | 14 | 100.0 | 152 | 3 | US-08-482-658-9 | Sequence 9, Appl |
| 36 | 14 | 100.0 | 152 | 3 | US-08-482-658-10 | Sequence 9, Appl |
| 37 | 14 | 100.0 | 152 | 3 | US-08-470-349-9 | Sequence 9, Appl |
| 38 | 14 | 100.0 | 152 | 3 | US-08-470-349-10 | Sequence 9, Appl |
| 39 | 14 | 100.0 | 152 | 3 | US-08-475-610-9 | Sequence 9, Appl |
| 40 | 14 | 100.0 | 152 | 3 | US-08-475-610-10 | Sequence 9, Appl |
| 41 | 14 | 100.0 | 152 | 5 | PCT-US92-00277-9 | Sequence 9, Appl |
| 42 | 14 | 100.0 | 152 | 5 | PCT-US92-00277-10 | Sequence 9, Appl |
| 43 | 14 | 100.0 | 152 | 5 | PCT-US92-00278-10 | Sequence 10, Appl |
| 44 | 14 | 100.0 | 153 | 5 | PCT-US92-00278-12 | Sequence 12, Appl |
| 45 | 14 | 100.0 | 154 | 1 | US-08-090-193-12 | Sequence 12, Appl |

ALIGNMENTS

RESULT 1
US-08-090-193-14
Sequence 14, Application US/08090193
Patent No. 5641673
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5641673bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,193
FILING DATE: 23-DEC-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalà, Michele A.
REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0609.3080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-090-193-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-857-841-4 (1-14) x US-08-090-193-14 (1-130)

Qy 1 MetApLySeRgIuSeRThSeRlAgLyArGaMaRgArG 14
Db 53 ATGACAAATCTGAATCAACCACTGCTGCTAACCCTCGA 94

RESULT 2
US-08-488-031-14
Sequence 14, Application US/08488031
Patent No. 5849548
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5849548bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,031
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080002/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both

TOPOLOGY: linear
US-08-488-031-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-031-14 (1-130)

Qy 1 MetApLySeRgIuSeRThSeRlAgLyArGaMaRgArG 14
Db 53 ATGACAAATCTGAATCAACCACTGCTGCTAACCCTCGA 94

RESULT 3
US-08-486-569-14
Sequence 14, Application US/08486569
Patent No. 5863774
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5863774bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,569
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080006/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-486-569-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-486-569-14 (1-130)

QY 1 MetApIySserGIuSerThSer1AglYArGaAnaGarg 14
Db 53 ATGACAAATCTGAATCAACCAAGTCTGTCGTAAACCTCGA 94

RESULT 4

US-08-488-027-14
; Sequence 14, Application US/08488027
; Patent No. 5866384
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea, 5866384bert
; APPLICANT: Perimon, No. 5866384bert
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,027
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/090,193
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00277
; FILING DATE: 16-JAN-1992
; APPLICATION NUMBER: US 07/642,330
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609,3080003/MAC/LBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
US-08-488-027-14

Alignment Scores:

| Pred. No.: | 3,32e-06 | Length: | 130 |
|------------------------|----------|---------------|-----|
| Score: | 14.00 | Matches: | 14 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-09-857-841-4 (1-14) x US-08-488-027-14 (1-130)

QY 1 MetApIySserGIuSerThSer1AglYArGaAnaGarg 14
Db 53 ATGACAAATCTGAATCAACCAAGTCTGTCGTAAACCTCGA 94
RESULT 5

US-08-090-192-14
; Sequence 14, Application US/08090192
; Patent No. 5874414
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Goodman, Howard M.
; TITLE OF INVENTION: Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/090,192
; FILING DATE: 11-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/ US 92/00278
; FILING DATE: 16-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/642,333
; FILING DATE: 17-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbal, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0609,3030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
US-08-090-192-14

Alignment Scores:

| Pred. No.: | 3,32e-06 | Length: | 130 |
|------------------------|----------|---------------|-----|
| Score: | 14.00 | Matches: | 14 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-09-857-841-4 (1-14) x US-08-090-192-14 (1-130)

QY 1 MetApIySserGIuSerThSer1AglYArGaAnaGarg 14
Db 53 ATGACAAATCTGAATCAACCAAGTCTGTCGTAAACCTCGA 94

RESULT 6

US-08-482-663-14
; Sequence 14, Application US/08482663
; Patent No. 5882907
; GENERAL INFORMATION:
; APPLICANT: Haseloff, James
; APPLICANT: Brand, Andrea
; APPLICANT: Perimon, No. 5882907bert
; TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/482,663
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609,3080005/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-482-663-14

Alignment Scores:
Seq. No.: 3,32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-482-663-14 (1-130)

RESULT 7
US-08-482-658-14
Sequence 14, Application US/08482658
Patent No. 6010904
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Bertrmon, No. 6010904bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609,3080008/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-482-658-14

Alignment Scores:
Seq. No.: 3,32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-857-841-4 (1-14) x US-08-482-658-14 (1-130)

RESULT 8
US-08-470-349-14
Sequence 14, Application US/08470349
Patent No. 6015794
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,349
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,192
FILING DATE: 11-NOV-1993
APPLICATION NUMBER: PCT/ US 92/00278
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,333

FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimble, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0609.3030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-470-349-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 3

US-09-857-841-4 (1-14) x US-08-470-349-14 (1-130)

Oy 1 MetApIySserGIuSerThrSerAlaGlyArgAnaArg 14
Db 53 ATGACAAATCTGAATCAACAGTGTGCTGTAACCGTGA 94

RESULT 9
US-08-475-610-14
Sequence 14, Application US/08475610
Patent No. 6071730
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perimon, No. 6071730bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,610
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080004/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-475-610-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 3

US-09-857-841-4 (1-14) x US-08-475-610-14 (1-130)

Oy 1 MetApIySserGIuSerThrSerAlaGlyArgAnaArg 14
Db 53 ATGACAAATCTGAATCAACAGTGTGCTGTAACCGTGA 94

RESULT 10
PCT-US92-00277-14
Sequence 14, Application PC/TUS9200277
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Goodman, Howard M.
APPLICANT: Brand, Andrea
APPLICANT: Perimon, Noibert
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Avenue, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 19920116
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3496604
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)833-7533
TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US92-00277-14

Alignment Scores:
Pred. No.: 3.32e-06 Length: 130
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 5

US-09-857-841-4 (1-14) X PCT-US92-00277-14 (1-130)

```
QY      1 MetAspIySergIuseRThrsEraIagIyArgasnaRgArc 14
          |||||
Db       53 ATGACAAATCTGAATCAACCAGTGTGTCTGTAACCGTCGA 94
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RESULT 11
PCT-US92-00278-14

; APPLICANT: Haseloff, James
 ; APPLICANT: Goodman, Howard M.
 ; TITLE OF INVENTION: Trans-Splicing Ribozymes
 ; NUMBER OF SEQUENCES: 51
 ; CORRESPONDENCE ADDRESS:

```

1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: PatentIn Release #1.0, Version #1.25
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: PCT/US92/00278
8 FILING DATE: 19920116

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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:

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MOLECULE TYPE: Nucleic Acid
PCT-US92-00278-14

| | |
|------------------------|----------|
| Alignment Scores: | |
| Pred. No.: | 3.32e-06 |
| Score: | 14.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 100.00% |
| DB: | 5 |
| Length: | 13 |
| Matches: | 14 |
| Conservative: | 0 |
| Mismatches: | 0 |
| Indels: | 0 |
| Gaps: | 0 |

US-09-857-841-4 (1-14) x PCT-US92-00278-14 (1-130)

QY 1 MetAspIyBSerGIuSerThrSerAlaGIyArGAsnArGArg 14
Db 53 ATGGAACAATCTGAATCAACCAAGTGTGTGTGTAACCGTCGA 94

RESULT 12
US-08-090-193-11

GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5641673bert
APPLICANT: Goodman, Howard M.

TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090.193
FILING DATE: 23-DEC-1993

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
8-090-193-11

US-08-090-193-11

| | |
|------------------------|----------|
| Argument Scores: | |
| Pred. No.: | 3.34e-06 |
| Score: | 14.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 100.00% |
| DB: | 1 |
| | |
| Length: | 13 |
| Matches: | 14 |
| Conservative: | 0 |
| Mismatches: | 0 |
| Indels: | 0 |
| Gaps: | 0 |

US-09-857-841-4 (1-14) X US-08-090-193-11 (1-131)

```
QY      1 MetAspIySSerGIuSerThrSerAlaGlyArgAsnArg 14
          |||||
Db       54 ATGACAATCTGATCAACCAAGTGCTGTGTTACCCTCGA 95
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RESULT 13
US-08-488-031-11
; Sequence 11, Application US/08488031
; Patent No. 5849548

APPLICANT: Haseloff, James
 APPLICANT: Brand, Andrea
 APPLICANT: Perrimon, No. 5849548bert
 APPLICANT: Goodman, Howard M.
 TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS:

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,031
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080002/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-488-031-11

Alignment Scores:
Pred. No.: 3,346-06 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-031-11 (1-131)

QY 1 MetAplySergiuSerThrSerAlaGlyArgAsnArg 14
DB 54 ATGACAAATCTGATCAACGAGTGTGTGCTAACCGTCA 95

RESULT 14
US-08-486-569-11
Sequence 11, Application US/08486569
Patent No. 5863774
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5863774bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,569
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3080006/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-486-569-11

Alignment Scores:
Pred. No.: 3,346-06 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-486-569-11 (1-131)

QY 1 MetAplySergiuSerThrSerAlaGlyArgAsnArg 14
DB 54 ATGACAAATCTGATCAACGAGTGTGTGCTAACCGTCA 95

RESULT 15
US-08-488-027-11
Sequence 11, Application US/08488027
Patent No. 5866384
GENERAL INFORMATION:
APPLICANT: Haseloff, James
APPLICANT: Brand, Andrea
APPLICANT: Perrimon, No. 5866384bert
APPLICANT: Goodman, Howard M.
TITLE OF INVENTION: Cell Ablation Using Trans-Splicing Ribozymes
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,027
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/090,193
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00277
FILING DATE: 16-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/642,330
FILING DATE: 17-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086

REFERENCE/DOCKET NUMBER: 0609.3080003/MAC/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
US-08-488-027-11

Alignment Scores:
Pred. No.: 3.34e-06 Length: 131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-857-841-4 (1-14) x US-08-488-027-11 (1-131)

Qy 1 MetAplysSergLuserThSerAaglyAgaAenAarg 14
|||
Db 54 ATGACAAATCTGATCAACCGAGTGTGTCGTAAACGTCGA 95

Search completed: December 5, 2004, 11:11:50
Job time : 68 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2004, 09:48:28 ; Search time 351 Seconds

(without alignments)
219.166 Million cell updates/sec

Title: US-09-857-841-4

Perfect score: 14

Sequence: 1 MDKSESTAGNNRR 14

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3694831 seqs, 2747406616 residues

Word size: 1

Total number of hits satisfying chosen parameters: 7376254

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.epool/US09857841/runat_03122004_160614_19170/app.query.fasta_1.199
-DB=Published Applications NA -PFMT=fastcap -SUFFIX=olip2n.rmpb -MINMATCH=0.1
-LOOCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=prco -NORM=ext -HEAPSIZ=500 -MUTLEN=0
-MAXLEN=2000000000 -USER=US09857841@cgn2_1_480@runat_03122004_160614_19170
-NCPU=6 -ICPU=3 -NO NMAP -LANG=QUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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17: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 14 | 100.0 | 771 | 13 | US-10-011-033-5 |
| 2 | 14 | 100.0 | 772 | 13 | US-10-011-033-1 |
| 3 | 14 | 100.0 | 772 | 13 | US-10-011-033-14 |
| 4 | 14 | 100.0 | 792 | 13 | US-10-011-033-3 |
| 5 | 12 | 85.7 | 960 | 13 | US-10-011-033-9 |
| 6 | 8 | 57.1 | 792 | 17 | US-10-437-963-3120 |
| 7 | 7 | 50.0 | 107 | 16 | US-10-424-599-140904 |
| 8 | 7 | 50.0 | 166 | 16 | US-10-425-115-66023 |
| 9 | 7 | 50.0 | 233 | 16 | US-10-424-599-94618 |
| 10 | 7 | 50.0 | 279 | 9 | US-09-960-352-7184 |
| 11 | 7 | 50.0 | 316 | 18 | US-10-425-115-46484 |
| 12 | 7 | 50.0 | 408 | 10 | US-09-818-995-34460 |
| 13 | 7 | 50.0 | 452 | 9 | US-09-998-598-1555 |
| 14 | 7 | 50.0 | 464 | 9 | US-09-864-761-15219 |
| 15 | 7 | 50.0 | 478 | 18 | US-10-425-115-17482 |
| 16 | 7 | 50.0 | 509 | 13 | US-10-027-632-234457 |
| 17 | 7 | 50.0 | 509 | 13 | US-10-027-632-234457 |
| 18 | 7 | 50.0 | 518 | 15 | US-10-029-386-11750 |
| 19 | 7 | 50.0 | 563 | 16 | US-10-424-599-31741 |
| 20 | 7 | 50.0 | 570 | 15 | US-10-029-386-11368 |
| 21 | 7 | 50.0 | 627 | 18 | US-10-425-115-59660 |
| 22 | 7 | 50.0 | 654 | 15 | US-10-156-761-7305 |
| 23 | 7 | 50.0 | 715 | 18 | US-10-425-115-42949 |
| 24 | 7 | 50.0 | 726 | 15 | US-10-156-761-4748 |
| 25 | 7 | 50.0 | 747 | 18 | US-10-425-115-61326 |
| 26 | 7 | 50.0 | 819 | 15 | US-10-369-493-37738 |
| 27 | 7 | 50.0 | 852 | 16 | US-10-424-599-42689 |
| 28 | 7 | 50.0 | 855 | 15 | US-10-126-103-37 |
| 29 | 7 | 50.0 | 855 | 16 | US-10-431-096-37 |
| 30 | 7 | 50.0 | 902 | 16 | US-10-424-599-110979 |
| 31 | 7 | 50.0 | 936 | 16 | US-10-425-114-13812 |
| 32 | 7 | 50.0 | 1071 | 14 | US-10-198-846-10820 |
| 33 | 7 | 50.0 | 1138 | 10 | US-09-822-846-464 |
| 34 | 7 | 50.0 | 1323 | 15 | US-10-369-493-32000 |
| 35 | 7 | 50.0 | 1347 | 17 | US-10-437-963-67382 |
| 36 | 7 | 50.0 | 1467 | 15 | US-10-156-761-6326 |
| 37 | 7 | 50.0 | 1471 | 9 | US-09-764-869-455 |
| 38 | 7 | 50.0 | 1471 | 14 | US-10-091-504-455 |
| 39 | 7 | 50.0 | 1471 | 16 | US-10-227-577-455 |
| 40 | 7 | 50.0 | 1554 | 15 | US-10-369-493-35770 |
| 41 | 7 | 50.0 | 1566 | 15 | US-10-369-493-44194 |
| 42 | 7 | 50.0 | 1568 | 16 | US-10-343-710-78 |
| 43 | 7 | 50.0 | 1603 | 16 | US-10-282-1224-78385 |
| 44 | 7 | 50.0 | 1635 | 16 | US-10-282-1224-78233 |
| 45 | 7 | 50.0 | 1657 | 18 | US-10-425-115-138705 |

ALIGNMENTS

RESULT 1
US-10-011-033-5
Sequence 5, Application US/10011033

Publication No. US20020124286A1

GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F

TITLE OF INVENTION: Plantes Resistant to C Strains of

Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rockey, Milnamov & Katz, Ltd.

STREET: 2 Prudential Plaza, 180 N. Steetson, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60089

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber mosaic virus
STRAIN: V-34
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
OTHER INFORMATION: /codon_start=3
/function="ENCAPSIDATES VIRUS RNA"
/product="COAT PROTEIN"
/gene="Cp"
/number=1
/standard_name="COAT PROTEIN"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-011-033-5
Alignment Scores:
Pred. No.: 9.49e-06 Length: 771
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-5 (1-771)
Cy 1 MetApLySeRgIuSeRThSeRAlaGlyARgAsnARgArg 14
Db 3 ATGGACAAATCTGATCAACACGCTGCTGCTAACCGTCGA 44
RESULT 2
US-10-011-033-1
Sequence 1, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-No. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: V-27
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-011-033-1
Alignment Scores:
Pred. No.: 9.5e-06 Length: 772
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-1 (1-772)
Cy 1 MetApLySeRgIuSeRThSeRAlaGlyARgAsnARgArg 14
Db 3 ATGGACAAATCTGATCAACACGCTGCTGCTAACCGTCGA 44
RESULT 3
US-10-011-033-14
Sequence 14, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011.033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875.233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cucumber Mosaic Virus
INDIVIDUAL ISOLATE: A35
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-011-033-14
Alignment Scores:
Pred. No.: 9.5e-06 Length: 772
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-14 (1-772)
Oy 1 MetAspLySeRgJuseRThSeRAlaGlyARgAsnARgArg 14
Db 3 ATGGACAAATCTGATCAACGAGTCTGTCGTACCGTCA 44
RESULT 4
US-10-011-033-3
Sequence 3, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rockey, Milanow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011.033
FILING DATE: 13-NO. US20020124286A1-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875.233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: V-33
FEATURE:
NAME/KEY: CDS
LOCATION: 3..660
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-011-033-3
Alignment Scores:
Pred. No.: 9.7e-06 Length: 792
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-857-841-4 (1-14) x US-10-011-033-3 (1-792)
Oy 1 MetAspLySeRgJuseRThSeRAlaGlyARgAsnARgArg 14
Db 3 ATGGACAAATCTGATCAACGAGTCTGTCGTACCGTCA 44
RESULT 5
US-10-011-033-9
Sequence 9, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rockey, Milanow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011.033
FILING DATE: 13-NO. US20020124286A1-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875.233
FILING DATE: 26-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: CUCUMBER MOSAIC VIRUS
STRAIN: STRAIN C

FEATURE:
NAME/KEY: CDS
LOCATION: 1..658
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-011-033-9

Alignment Scores:
Pred. No.: 0.00135 Length: 960
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.71% Indels: 0
DB: 13 Gaps: 0

US-09-857-841-4 (1-14) x US-10-011-033-9 (1-960)

Oy 1 MetApLySeRgLuSeThrSeRaLaGlyArgAsn 12
DB 1 ATGGACAATCTGAATCAACGAGTCTGTCGTAAAC 36

RESULT 6
US-10-437-963-3120
; Sequence 3120, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 3120
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102831C.1
US-10-437-963-3120

Alignment Scores:
Pred. No.: 16.4 Length: 792
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 17 Gaps: 0

US-09-857-841-4 (1-14) x US-10-437-963-3120 (1-792)

Oy 4 SerGluSerThrSerAlaGlyArg 11
DB 734 TCGAGAGACACTCAGCTGGGCCG 757

RESULT 7
US-10-424-599-140904
; Sequence 140904, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 140904
; LENGTH: 107
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_98246C.1
US-10-424-599-140904

Alignment Scores:
Pred. No.: 35.2 Length: 107
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 16 Gaps: 0

US-09-857-841-4 (1-14) x US-10-424-599-140904 (1-107)

Oy 3 LysSerGluSerThrSerAla 9
DB 54 AAATCAGATGCACTTCTGCT 74

RESULT 8
US-10-425-115-66023
; Sequence 66023, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 66023
; LENGTH: 166
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(166)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_160212C.1
US-10-425-115-66023

Alignment Scores:
Pred. No.: 50.3 Length: 166
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 18 Gaps: 0

US-09-857-841-4 (1-14) x US-10-425-115-66023 (1-166)

OY 8 SerAlaGlyArgAsnArgArg 14
DB 56 AGTGGCGGAGAGAAATGAGAG 76

RESULT 9

US-10-424-599-94618
Sequence 94618, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic David K.
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 94618
LENGTH: 233
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_56451C.1
US-10-424-599-94618

Alignment Scores:

Pred. No.: 66.3 Length: 233
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 16 Gaps: 0

US-09-857-841-4 (1-14) x US-10-424-599-94618 (1-233)

OY 7 ThSerAlaGlyArgAsnArg 13
DB 85 ACCAGCGCGGAGAGAACAGA 105

RESULT 10

US-09-960-352-7184
Sequence 7184, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Mengping
APPLICANT: Byatt, John C.
APPLICANT: Mathiasen, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 7184
LENGTH: 279
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 31-LIB3057-014-Q1-K1-H3
US-09-960-352-7184

Alignment Scores:
Pred. No.: 76.8 Length: 279
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 9 Gaps: 0

US-09-857-841-4 (1-14) x US-09-960-352-7184 (1-279)

OY 7 ThSerAlaGlyArgAsnArg 13
DB 131 ACATCAGCAGACCGAACCGT 151

RESULT 11

US-10-425-115-46484
Sequence 46484, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 46484
LENGTH: 316
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_142399C.1
US-10-425-115-46484

Alignment Scores:

Pred. No.: 85 Length: 316
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 18 Gaps: 0

US-09-857-841-4 (1-14) x US-10-425-115-46484 (1-316)

OY 3 ThSerGlySerThSerAla 9
DB 161 AAGAGCGAGACGACGTACGCC 181

RESULT 12

US-09-918-995-34460
Sequence 34460, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 34460
LENGTH: 408
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-995-34460

Alignment Scores:
Pred. No.: 105 Length: 408
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00%

Query Match: 50.00% Indels: 0
DB: 10 Gaps: 0

US-09-857-841-4 (1-14) x US-09-918-995-34460 (1-408)

QY 8 SerAlagIaGaaAaGATG 14
DB 143 TCGGCTGGAAGAAATCGGAGG 163

RESULT 13
US-09-998-598-1555/C
Sequence 1555, Application US/09998598
Patent No. US20020150922A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Mesgher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 1555
LENGTH: 452
TYPE: DNA
ORGANISM: Homo sapiens
US-09-998-598-1555

Alignment Scores:
Pred. No.: 114 Length: 452
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
Gaps: 0

US-09-857-841-4 (1-14) x US-09-998-598-1555 (1-452)

QY 5 GluSerThrSerAlaGlyArg 11
DB 87 GAGTCGACGTCACGCGGAAGG 67

RESULT 14
US-09-864-761-15219
Sequence 15219, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
SEQ ID NO 15219
LENGTH: 464
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011288.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
US-09-864-761-15219

Alignment Scores:
Pred. No.: 116 Length: 464
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
Gaps: 0

US-09-857-841-4 (1-14) x US-09-864-761-15219 (1-464)

QY 4 SerGluSerThrSerAlaGly 10
DB 38 TCAGAAAGCACTCAGCTGGT 58

RESULT 15
US-10-425-115-174482/C
Sequence 174482, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 174482
LENGTH: 478
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_90708C.1
US-10-425-115-174482

Alignment Scores:
Pred. No.: 119 Length: 478
Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 18 Gaps: 0

US-09-857-841-4 (1-14) x US-10-425-115-174482 (1-478)

Oy 4 SerGIuSerThrSerAlaGly 10
|||||
243 TCGAAGACACGTGCGCAGGT 223

Search completed: December 5, 2004, 11:17:49
Job time : 353 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compu

ein Search, using sw model

December 5, 2004, 08:14:04 ; Search time 66 Seconds
(without attachments)

75.647 Million cell updates/sec

S-09-857-841-4

MDKSESTSAGRNR 14

LIGO

582122 reqs, 356623098 residues

its satisfying chosen parameters:

length: 2000000000

Listing first 45 summaries

Published Applications AA: *

Published Applications AA.*

1. /cgn2 6/ptodata/2/pubpaa/US07_PUBCOMB.dep.*
2. /cgn2 6/ptodata/2/pubpaa/PTU5_NEW_PUB.dep.*
3. /cgn2 6/ptodata/2/pubpaa/US06_NEW_PUB.dep.*
4. /cgn2 6/ptodata/2/pubpaa/US05_PUBCOMB.dep.*
5. /cgn2 6/ptodata/2/pubpaa/US07_NEW_PUB.dep.*
6. /cgn2 6/ptodata/2/pubpaa/PTU5_PUBCOMB.dep.*
7. /cgn2 6/ptodata/2/pubpaa/US08_NEW_PUB.dep.*
8. /cgn2 6/ptodata/2/pubpaa/US08_PUBCOMB.dep.*
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10. /cgn2 6/ptodata/2/pubpaa/US09_PUBCOMB.dep.*
11. /cgn2 6/ptodata/2/pubpaa/US09_PUBCOMB.dep.*
12. /cgn2 6/ptodata/2/pubpaa/US09_NEW_PUB.dep.*
13. /cgn2 6/ptodata/2/pubpaa/US10_PUBCOMB.dep.*
14. /cgn2 6/ptodata/2/pubpaa/US10_PUBCOMB.dep.*
15. /cgn2 6/ptodata/2/pubpaa/US10_PUBCOMB.dep.*
16. /cgn2 6/ptodata/2/pubpaa/US10_NEW_PUB.dep.*
17. /cgn2 6/ptodata/2/pubpaa/US10_NEW_PUB.dep.*
18. /cgn2 6/ptodata/2/pubpaa/US11_NEW_PUB.dep.*
19. /cgn2 6/ptodata/2/pubpaa/US60_NEW_PUB.dep.*
20. /cgn2 6/ptodata/2/pubpaa/US60_PUBCOMB.dep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------------------|------------------------|
| 1 | 14 | 100.0 | 218 | 13 | US-10-011-033-2 | Sequence 2, Appl1 |
| 2 | 14 | 100.0 | 218 | 13 | US-10-011-033-4 | Sequence 4, Appl1 |
| 3 | 14 | 100.0 | 218 | 13 | US-10-011-033-6 | Sequence 6, Appl1 |
| 4 | 14 | 100.0 | 218 | 13 | US-10-011-033-15 | Sequence 15, Appl1 |
| 5 | 12 | 85.7 | 218 | 13 | US-10-011-033-10 | Sequence 10, Appl1 |
| 6 | 7 | 50.0 | 183 | 15 | US-10-424-599-283746 | Sequence 283746, Appl1 |
| 7 | 7 | 50.0 | 183 | 15 | US-10-425-114-51049 | Sequence 51049, Appl1 |
| 8 | 7 | 50.0 | 343 | 15 | US-10-425-114-53499 | Sequence 53499, Appl1 |
| 9 | 7 | 50.0 | 375 | 17 | US-10-425-115-32368 | Sequence 32368, Appl1 |
| 10 | 7 | 50.0 | 448 | 16 | US-10-437-963-169865 | Sequence 169865, Appl1 |
| 11 | 7 | 50.0 | 469 | 15 | US-10-424-599-236497 | Sequence 236497, Appl1 |
| 12 | 6 | 42.9 | 15 | 16 | US-10-203-915A-131 | Sequence 131, Appl1 |
| 13 | 6 | 42.9 | 15 | 16 | US-10-203-915A-132 | Sequence 132, Appl1 |

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|----|---|------|-------|----|----------------------|--------------------------|
| 14 | 6 | 42.9 | 13.15 | 16 | US-10-603-9158-1341 | Sequence 133, App |
| 15 | 5 | 42.9 | 54 | 15 | US-10-624-599-145411 | Sequence 145411, |
| 16 | 6 | 42.9 | 65 | 17 | US-10-425-115-311170 | Sequence 311170, |
| 17 | 6 | 42.9 | 68 | 17 | US-10-425-115-288412 | Sequence 288412, |
| 18 | 6 | 42.9 | 78 | 15 | US-10-424-599-256382 | Sequence 256382, |
| 19 | 6 | 42.9 | 81 | 17 | US-10-425-115-352829 | Sequence 352829, |
| 20 | 6 | 42.9 | 83 | 15 | US-10-424-599-145321 | Sequence 145321, |
| 21 | 6 | 42.9 | 85 | 17 | US-10-425-115-311232 | Sequence 311232, |
| 22 | 6 | 42.9 | 85 | 17 | US-10-425-115-206505 | Sequence 206505, |
| 23 | 6 | 42.9 | 91 | 17 | US-10-425-115-244053 | Sequence 244053, |
| 24 | 6 | 42.9 | 98 | 17 | US-10-425-115-356957 | Sequence 356957, |
| 25 | 6 | 42.9 | 100 | 16 | US-10-437-963-103201 | Sequence 103201, |
| 26 | 6 | 42.9 | 105 | 16 | US-10-437-963-177629 | Sequence 177629, |
| 27 | 6 | 42.9 | 107 | 17 | US-10-425-115-291239 | Sequence 291239, |
| 28 | 6 | 42.9 | 126 | 15 | US-10-425-115-59079 | Sequence 59079, <i>P</i> |
| 29 | 6 | 42.9 | 127 | 16 | US-10-437-963-124842 | Sequence 124842, |
| 30 | 6 | 42.9 | 131 | 16 | US-10-437-963-105655 | Sequence 105655, |
| 31 | 6 | 42.9 | 135 | 15 | US-10-425-114-58305 | Sequence 58305, <i>P</i> |
| 32 | 6 | 42.9 | 142 | 16 | US-10-437-963-110739 | Sequence 110739, |
| 33 | 6 | 42.9 | 156 | 16 | US-10-437-963-121791 | Sequence 121791, |
| 34 | 6 | 42.9 | 160 | 17 | US-10-425-115-261076 | Sequence 261076, |
| 35 | 6 | 42.9 | 168 | 15 | US-10-425-114-39432 | Sequence 39432, <i>P</i> |
| 36 | 6 | 42.9 | 171 | 17 | US-10-425-115-330960 | Sequence 330960, |
| 37 | 6 | 42.9 | 176 | 17 | US-10-425-115-284516 | Sequence 284516, |
| 38 | 6 | 42.9 | 199 | 16 | US-10-437-963-196177 | Sequence 196177, |
| 39 | 6 | 42.9 | 202 | 16 | US-10-437-963-110737 | Sequence 110737, |
| 40 | 6 | 42.9 | 223 | 14 | US-10-369-993-19842 | Sequence 19842, <i>P</i> |
| 41 | 6 | 42.9 | 240 | 15 | US-10-282-1224-70451 | Sequence 70451, <i>P</i> |
| 42 | 6 | 42.9 | 250 | 17 | US-10-425-115-236535 | Sequence 236535, |
| 43 | 6 | 42.9 | 251 | 15 | US-10-425-114-39110 | Sequence 39110, <i>P</i> |
| 44 | 6 | 42.9 | 263 | 16 | US-10-408-1654-2608 | Sequence 2608, <i>P</i> |
| 45 | 6 | 42.9 | 272 | 17 | US-10-425-115-287096 | Sequence 287096, |

ALIGNMENTS

RESULT 1
US-10-011-033-2

REAL INFORMATION:

McMaster, J. Russell

Reynolds, John F

TITLE OF INVENTION: Plants Resistant to C Strains of

NUMBER OF SEQUENCES: 15

ADDRESSEE: Rocky, Milnamow & Katz, Ltd.

CITY: Chicago

COUNTRY: U.S.A.
ZTD: 60090

COMPUTER READABLE FORM:
MEDIUM TYPE: P3001

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/011, 033
FILING DATE: 13-NOV-2001

CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 05/08/813,235
FILING DATE: 26-JUN-1997

ALLORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-011-033-2

Query Match 100.0%; Score 14; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14

RESULT 2

US-10-011-033-4
Sequence 4, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-011-033-4

Query Match 100.0%; Score 14; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14

RESULT 3
US-10-011-033-6
Sequence 6, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-011-033-6

Query Match 100.0%; Score 14; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGRNR 14
DB 1 MDKSESTSGRNR 14

RESULT 4

US-10-011-033-15
Sequence 15, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
Cucumber Mosaic Virus

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago

STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-011-033-15

Query Match 100.0%; Score 14; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 2,2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGNRR 14
|||||
1 MDKSESTSAGNRR 14

Db

RESULT 5
US-10-011-033-10
Sequence 10, Application US/10011033
Publication No. US20020124286A1
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L.
McMaster, J. Russell
Tricoli, David M
Reynolds, John F
Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,033
FILING DATE: 13-NO. US20020124286A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-011-033-10

Query Match 85.7%; Score 12; DB 13; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRN 12
|||||
1 MDKSESTSAGRN 12

Db

RESULT 6
US-10-424-599-283746
Sequence 283746, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 283746
SEQ ID NO 283746
LENGTH: 35
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_98246C.1.pcp
US-10-424-599-283746

Query Match 50.0%; Score 7; DB 15; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KSESTSA 9
|||||
18 KSESTSA 24

Db

RESULT 7
US-10-425-114-51049
Sequence 51049, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53113)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 51049
LENGTH: 183
TYPE: PRT
ORGANISM: Zea mays

FEATURE:
OTHER INFORMATION: Clone ID: L1B143-062-F2_F11.pep
US-10-425-114-51049

Query Match 50.0%; Score 7; DB 15; Length 183;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ESTSAGR 11
|||||
DB 84 ESTSAGR 90

RESULT 8
US-10-425-114-53499
Sequence 53499, Application US/10425114
Publication No. US20040034688A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5313)B
CURRENT FILING DATE: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53499
LENGTH: 343
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700836661_F11.pep
US-10-425-114-53499

Query Match 50.0%; Score 7; DB 15; Length 343;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KSESTSA 9
|||||
DB 28 KSESTSA 34

RESULT 9
US-10-425-115-323368
Sequence 323368, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 323368
LENGTH: 375
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_57983C.1.pep
US-10-425-115-323368

Query Match 50.0%; Score 7; DB 17; Length 375;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ESTSAGR 11
|||||
DB 276 ESTSAGR 282

RESULT 10
US-10-437-963-169865
Sequence 169865, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bonkharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 169865
LENGTH: 448
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(448)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_68245C.1.pep
US-10-437-963-169865

Query Match 50.0%; Score 7; DB 16; Length 448;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ESTSAGR 11
|||||
DB 307 ESTSAGR 313

RESULT 11
US-10-424-599-236497
Sequence 236497, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 236497
LENGTH: 469
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_55584C.1.pep
US-10-424-599-236497

Query Match 50.0%; Score 7; DB 15; Length 469;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KSESTSA 9
|||||
Db 28 KSESTSA 34

RESULT 12

US-10-203-915A-131
; Sequence 131, Application US/10203915A
; Publication No. US20040106159A1
; GENERAL INFORMATION:
; APPLICANT: Kern, Florian
; TITLE OF INVENTION: Method for Antigen-Specific Stimulation of T
; FILE REFERENCE: 010266wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/203,915A
; CURRENT FILING DATE: 2002-08-15
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 131
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HCMV pp65
US-10-203-915A-131

Query Match 42.9%; Score 6; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 STSAGR 11
|||||
Db 10 STSAGR 15

RESULT 13

US-10-203-915A-132
; Sequence 132, Application US/10203915A
; Publication No. US20040106159A1
; GENERAL INFORMATION:
; APPLICANT: Kern, Florian
; TITLE OF INVENTION: Method for Antigen-Specific Stimulation of T
; FILE REFERENCE: 010266wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/203,915A
; CURRENT FILING DATE: 2002-08-15
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HCMV pp65
US-10-203-915A-132

Query Match 42.9%; Score 6; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 STSAGR 11
|||||
Db 6 STSAGR 11

RESULT 14
US-10-203-915A-133
; Sequence 133, Application US/10203915A
; Publication No. US20040106159A1
; GENERAL INFORMATION:
; APPLICANT: Kern, Florian

; TITLE OF INVENTION: Method for Antigen-Specific Stimulation of T
; FILE REFERENCE: 010266wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/203,915A
; CURRENT FILING DATE: 2002-08-15
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HCMV pp65
US-10-203-915A-133

Query Match 42.9%; Score 6; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 STSAGR 11
|||||
Db 2 STSAGR 7

RESULT 15

US-10-424-599-145411
; Sequence 145411, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 145411
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102325C.1.pap
US-10-424-599-145411

Query Match 42.9%; Score 6; DB 15; Length 54;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSES 6
|||||
Db 1 MDKSES 6

Search completed: December 5, 2004, 08:19:00
Job time : 67 secs

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OM protein - protein search, using sw model

Run on: December 5, 2004, 08:05:52 ; Search time 92 Seconds
(without alignments)
87.557 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 14
Sequence: 1 MDKSESTSAGNR 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Uniprot 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 2 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 3 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 4 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 5 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 6 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 7 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 8 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 9 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 10 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 11 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 12 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 13 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 14 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 15 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 16 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 17 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 18 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 19 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 20 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 21 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 22 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 23 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 24 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 25 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 26 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 27 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 28 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 29 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 30 | 14 | 100.0 | 217 | 2 | Q6T7D4 |
| 31 | 14 | 100.0 | 217 | 2 | Q6T7D4 |

| | | | | | |
|----|----|-------|-----|---|--------|
| 32 | 14 | 100.0 | 218 | 2 | Q76U37 |
| 33 | 14 | 100.0 | 218 | 2 | Q7TD9 |
| 34 | 14 | 100.0 | 218 | 2 | Q7TD9 |
| 35 | 14 | 100.0 | 218 | 2 | Q7TD9 |
| 36 | 14 | 100.0 | 218 | 2 | Q7TD9 |
| 37 | 14 | 100.0 | 218 | 2 | Q7TD9 |
| 38 | 14 | 100.0 | 218 | 2 | Q7TD9 |
| 39 | 14 | 100.0 | 218 | 2 | Q7TD9 |
| 40 | 14 | 100.0 | 218 | 2 | Q7TD9 |
| 41 | 14 | 100.0 | 218 | 2 | Q7TD9 |
| 42 | 14 | 100.0 | 218 | 2 | Q7TD9 |
| 43 | 14 | 100.0 | 218 | 2 | Q7TD9 |
| 44 | 14 | 100.0 | 218 | 2 | Q7TD9 |
| 45 | 14 | 100.0 | 218 | 2 | Q7TD9 |

ALIGNMENTS

| | | | | | |
|-----------------------|---|--------------|------|---------|--|
| RESULT 1 | | | | | |
| ID | Q6T7D4 | PRELIMINARY; | PRT; | 217 AA. | |
| AC | Q6T7D4 | | | | |
| DT | 05-JUL-2004 (TREMblrel. 27, Created) | | | | |
| DT | 05-JUL-2004 (TREMblrel. 27, Last sequence update) | | | | |
| DT | 05-JUL-2004 (TREMblrel. 27, Last annotation update) | | | | |
| DE | Coat protein. | | | | |
| OS | Cucumber mosaic virus (cucumber mosaic cucumovirus). | | | | |
| OC | Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae; | | | | |
| OC | Cucumovirus. | | | | |
| OX | NCBI_Taxid=12305; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RA | Yan L., Xu Z., Goldbach R., Chen K., Prins M. | | | | |
| RL | Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases. | | | | |
| DR | EMBL; AY429437; AAR89478.1; - | | | | |
| DR | GO; GO:0019028; C:Viral capsid; IEA. | | | | |
| DR | GO; GO:0005198; F:Structural molecule activity; IEA. | | | | |
| DR | InterPro; IPR000247; Cucumovirus_coat. | | | | |
| DR | InterPro; IPR008975; Viral_cap_coat. | | | | |
| DR | Pfam; PF00760; Cucumo_coat; 1. | | | | |
| DR | PRINTS; PR00222; CUCUMOCOAT. | | | | |
| DR | ProDom; PD001284; Cucumovirus_coat; 1. | | | | |
| KW | Coat protein. | | | | |
| SEQ | SEQUENCE 217 AA; 24015 MW; 32D0035B4F20B891 CRC64; | | | | |
| Query Match | 100.0%; Score 14; DB 2; Length 217; | | | | |
| Best Local Similarity | 100.0%; Pred. No. 3.6e-07; | | | | |
| Matches | 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | |
| OY | 1 MDKSESTSAGNR 14 | | | | |
| DB | 1 MDKSESTSAGNR 14 | | | | |
| RESULT 2 | | | | | |
| ID | Q66133 | PRELIMINARY; | PRT; | 217 AA. | |
| AC | Q66133 | | | | |
| DT | 01-NOV-1996 (TREMblrel. 01, Created) | | | | |
| DT | 01-NOV-1996 (TREMblrel. 01, Last sequence update) | | | | |
| DT | 01-OCT-2003 (TREMblrel. 25, Last annotation update) | | | | |
| DE | Coat protein. | | | | |
| OS | Cucumber mosaic virus (cucumber mosaic cucumovirus). | | | | |
| OC | Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae; | | | | |
| OC | Cucumovirus. | | | | |
| OX | NCBI_Taxid=12305; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RA | Reichel H., Martino L., Kummert J., Belalcazar S., Narvaez J.; | | | | |
| RT | "Caracterización del gen de la proteína de la capsida de los | | | | |
| RT | atañamientos del virus del mosaico del pepino (CMV), obtenidos de | | | | |
| RT | platano y banana (Musa spp.)."; | | | | |

```
RL Revista Corpoica 1:1-5(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Martino-Ramirez L.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U32859; AAB50176.1; -.
DR PIR; JC6073; JC6073.
DR PIR; JC6075; JC6075.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 217 AA; 24015 MW; 7251B7BE67192DCAB CRC64;

Query Match 100.0%; Score 14; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGAGNRR 14
DB 1 MDKSESTSGAGNRR 14

RESULT 3
OQ07AO PRELIMINARY; PRT; 217 AA.
AC OQ07AO;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Coat protein.
OS Banana mosaic virus.
OC Viruses; unclassified viruses.
OX NCBI_TaxID=179820;
RN [1]
RP SEQUENCE FROM N.A.
RA Daolin D., Jie S., Peng Z., Zhixin L., Xiaodong D., Xueqing Z.;
RL "Cloning and Reconstruction of a Expression Vector for the Banana
Mosaic Virus Coat Protein Gene.";
RL Guangxi Zhi Wu 0:0-0(2002).
DR EMBL; AF444252; AAL48223.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 217 AA; 23739 MW; 3873A80567D3B3AE CRC64;

Query Match 100.0%; Score 14; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGAGNRR 14
DB 1 MDKSESTSGAGNRR 14

RESULT 4
AAR89478 PRELIMINARY; PRT; 217 AA.
AC AAR89478;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Coat protein.
OS Cucumber mosaic virus (cucumber mosaic cucumovirus).
SQ
```

```
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=12305;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CS;
RA Yan L., Xu Z., Goldbach R., Chen K., Prins M.;
RT "Complete nucleotide sequence of cucumber mosaic virus (CS isolate)
RNA3 ";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY429437; AAR89478.1; -.
KW Coat protein.
SQ SEQUENCE 217 AA; 24015 MW; 32D0035B4F20E891 CRC64;

Query Match 100.0%; Score 14; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGAGNRR 14
DB 1 MDKSESTSGAGNRR 14

RESULT 5
COAT_CMVAS STANDARD; PRT; 218 AA.
AC Q66154;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumber mosaic virus (strain As) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117118;
RN [1]
RP SEQUENCE FROM N.A.
RA Hyon S., Park Y.I.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
family.
-----
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-----
DR EMBL; X77855; CA54846.1; -.
DR PIR; S42098; S42098.
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24044 MW; E6BEC3ED4CD73HF CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGAGNRR 14
DB 1 MDKSESTSGAGNRR 14

RESULT 6
COAT_CMVBA STANDARD; PRT; 218 AA.
ID COAT_CMVBA
AC Q66135;
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DR EMBL: D42079; BAA07675.1; -.
DR InterPro: IPR000247; Cucumovirus_coat.
DR InterPro: IPR008975; Viral_cap_coat.
DR Pfam: PF00760; Cucumo_coat; 1.
DR PRINTS: PR00222; CUCUMOCOAT.
DR ProDom: PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 2403 MW; 16D96022D1A26FD8 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGAGNRR 14
   |||||
Db 1 MDKSESTSGAGNRR 14

RESULT 8
COAT_CWVCS STANDARD; PRT; 218 AA.
AC Q66143;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DS Coat protein (Capsid protein) (CP).
OS Cucumber mosaic virus (strain CS) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117109;
RN [1]
RP SEQUENCE FROM N.A.
RA Chaumpluk P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,
RA Suuki K., Mise K., Inoue N., Okuno T., Furubawa I.;
RT "Six new subgroup I members of Japanese cucumber mosaic virus as
RT determined by nucleotide sequence analysis on RNA3' e cDNAs.";
RL Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).
RL -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
family.
-----
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CC EMBL: D28489; BAA05851.1; -.
DR InterPro: IPR000247; Cucumovirus_coat.
DR InterPro: IPR008975; Viral_cap_coat.
DR Pfam: PF00760; Cucumo_coat; 1.
DR PRINTS: PR00222; CUCUMOCOAT.
DR ProDom: PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24157 MW; 76F6BD9628F683 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGAGNRR 14
   |||||
Db 1 MDKSESTSGAGNRR 14

RESULT 9
COAT_CWVFC STANDARD; PRT; 218 AA.
AC Q00259;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

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CC CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, D10544; BA001403.1; -.
CC PIR, J01253; J01253.
CC InterPro, IPR000247; Cucumovirus_coat.
CC InterPro, IPR008975; Viral_cap_coat.
CC Pfam, PF00760; Cucumo_coat; 1.
CC PRINTS, PR00222; CUCUMOCOAT.
CC ProDom, PD001284; Cucumovirus_coat; 1.
CC KW Coat protein.
SQ SEQUENCE 218 AA; 24130 MW; C4B7CB12F2A7CAB CRC64;
OY Query Match 100.0%; Score 14; DB 1; Length 218;
Db Best Local Similarity 100.0%; Pred. No. 3,7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MDKSESTSGAGNRR 14
1 MDKSESTSGAGNRR 14
RESULT 10
COAT_CWVF
ID COAT_CWVF STANDARD; PRT; 218 AA.
AC Q66140;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumber mosaic virus (strain FT) (CMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117112;
OX [1]
RN SEQUENCE FROM N.A.
RP Chaumoulu P., Sasaki Y., Nakajima N., Nagano H., Nakamura I.,
RA Suzuki K., Mise K., Inoue N., Okuno T., Furusawa I.,
RT "Six new subgroup I members of Japanese cucumber mosaic virus as
determined by nucleotide sequence analysis on RNAs' s cDNAs.";
RL Ann. Phytopathol. Soc. Jpn. 62:40-44(1996).
RL -1. SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
family.
CC -----
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CC -----
CC EMBL, D28487; BA005847.1; -.
CC InterPro, IPR000247; Cucumovirus_coat.

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DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24160 MW; 5D3B98298EA3997 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 37e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGAGNRR 14
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Db 1 MDKSESTSGAGNRR 14

RESULT 11
COAT_CMV11 STANDARD; PRT; 218 AA.
AC P14767;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP). (CMV).
OS Cucumovirus mosaic virus (strain I17F) (CMV).
OC Virusae; ssRNA positive-strand virusae, no DNA stage; Bromoviridae;
OC Cucumovirus.
NCBI_TaxID=12308, 12307;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=I17F;
RC MEDLINE=90098885; PubMed=2602158;
RA Noel M.J.T., Ben Tahar S.;
RT "Nucleotide sequence of the coat protein gene and flanking regions of
RT Cucumovirus mosaic virus (CMV) strain I17F.";
RT Nucleic Acids Res. 17:10492-10492(1989).
[2]
RN ERRATUM.
RP MEDLINE=90206832; PubMed=2320436;
RA Noel M.J.T., Ben Tahar S.;
RL Nucleic Acids Res. 18:1332-1332(1990).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=FN1;
RC MEDLINE=91037954; PubMed=2230731;
RA Owen J., Shintaku M., Aeschleman P., Tahar S., Palukaitis P.;
RT "Nucleotide sequence and evolutionary relationships of cucumber mosaic
RT virus (CMV) strains; CMV RNA 3.";
RT J. Gen. Virol. 71:2243-2249(1990).
[1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
family.
-----
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-----
CC EMBL; X16386; CAA34422.1; -.
CC EMBL; D10538; BAA01397.1; -.
CC PIR; S09663; S09663.
CC InterPro; IPR000247; Cucumovirus_coat.
CC InterPro; IPR008975; Viral_cap_coat.
CC Pfam; PF00760; Cucumo_coat; 1.
CC PRINTS; PR00222; CUCUMOCOAT.
CC ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24140 MW; C4B4FCB21F197F98 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;

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Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTAGRNRR 14
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1 MDKSESTAGRNRR 14

RESULT 12

COAT_CWVI STANDARD; PRT; 218 AA.

DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain Itzuka) (CMV).
OC Cucumoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117113;
RN [1]
RA SEQUENCE FROM N.A.
RA Karasawa A., Ito A., Okada I., Hase S., Ehara Y.,
RT "A possible role of RNA 2 of cucumber mosaic cucumovirus as a
RT determinant of infection phenotype on compeas."
RL Ann. Phytopathol. Soc. Jpn. 63:289-297(1997).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.

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DR EMBL; D16405; BAA03889.1; -
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24144 MW; 087CFBFCDB90B6EB CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTAGRNRR 14
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1 MDKSESTAGRNRR 14

RESULT 13

COAT_CWKO STANDARD; PRT; 218 AA.

DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain Koz) (CMV).
OC Cucumoviridae;
OC Cucumovirus.
OX NCBI_TaxID=117116;
RN [1]
RA SEQUENCE FROM N.A.
RA Kim S.J., Cho H.S., Yu J.S., Kwon C.S., Kwon S.Y., Park E.K.,
RA Paek K.H.,
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein

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DR EMBL; L36251; AAA46418.1; -
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24138 MW; 04A21106D3D43344 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTAGRNRR 14
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1 MDKSESTAGRNRR 14

COAT_CWVM STANDARD; PRT; 218 AA.

DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Coat protein (Capsid protein) (CP).
OS Cucumbe mosaic virus (strain M) (CMV).
OC Cucumoviridae;
OC Cucumovirus.
OX NCBI_TaxID=31718;
RN [1]
RA SEQUENCE FROM N.A.
RA MEDLINE=91037954; PubMed=2230731;
RA Owen J., Shintaku M., Aeschleman P., Tahar S., Palukaitis P.;
RT "Nucleotide sequence and evolutionary relationships of cucumber mosaic
RT virus (CMV) strains; CMV RNA 3.";
RL J. Gen. Virol. 71:2243-2249(1990).
CC -1- SIMILARITY: Belongs to the cucumoviruses/bromoviruses coat protein
CC family.

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DR EMBL; D10539; BAA01399.1; -
DR InterPro; IPR000247; Cucumovirus_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00760; Cucumo_coat; 1.
DR PRINTS; PR00222; CUCUMOCOAT.
DR ProDom; PD001284; Cucumovirus_coat; 1.
KW Coat protein.
SQ SEQUENCE 218 AA; 24243 MW; 75B0BFEB247C93D7 CRC64;

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTAGRNRR 14
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1 MDKSESTAGRNRR 14

Db 1 MDKSESTSAGRNR 14

RESULT 15
COAT CMV

| ID | COAT CMVN | STANDARD; | PRT; | 218 AA. |
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DT 15-DEC-1998 (Rel. 37, Created)

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| DT | 15-DEC-1998 | (Rel. 37, Last annotation update) |
| D1 | 13-DEC-1998 | (Rel. 37, Last sequence update) |

coat protein (capsid protein) (CP).
Cucumber mosaic virus (strain N) (CMV)
DE
OS

OC Viruses; ssRNA positive-strand viruses,

NCBI_TaxID=117123;

| BP | SEQUENCE FROM N.A. |
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| KM | [1] |

RA Chaumpluk P., Sasaki Y., Nakajima N., I
BA Suzuki K. Miso K. Inoue N. Okuno T

RT "Six new subgroup I members of Japanese

Ann. Phytopathol. Soc. Jpn. 62:40-44 (1996)

-1- SIMILAR: BELONGS TO THE CUCURBITACEAE family.

cc The SWISS-PROT entry is correct. It
cc -----

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entitled requires a license agreement

or send an email to license@15b-81b.ch,

DR EMBL; D28486; BAA05845.1; -.

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InterPro; IPR008975; Viral_cap_coat.
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DR PRINTS: PR00222: CUCUMOCOAT.

DR Prodom; PD001284; Cucumovirus_coat; 1.
KM Coat protein

SQ SEQUENCE 218 AA; 24078 MW; 0BA67C84

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| Query Match | 100.0%; Score 14 |
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DEBC LOCAL 100:00, FREQ: NO
Matches 14: Conservative 0: Mismatch

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[illegible]

Search completed: December 5, 2004, 08:16:55

Job time : 93 secs

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OM protein - protein search, using sw model

Run on: December 5, 2004, 08:08:02 ; Search time 22 Seconds
(without alignments)
42.202 Million cell updates/sec

Title: US-09-857-841-4
Sequence: 1 MDKSESTSGRNR 14

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size: 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Issued Patents AA:
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 14 | 100.0 | 217 | 6 | 5422259-2 |
| 2 | 14 | 100.0 | 218 | 1 | US-08-398-209-2 |
| 3 | 14 | 100.0 | 218 | 1 | US-08-398-209-4 |
| 4 | 14 | 100.0 | 218 | 2 | US-08-553-619B-3 |
| 5 | 14 | 100.0 | 218 | 2 | US-08-875-233-2 |
| 6 | 14 | 100.0 | 218 | 3 | US-08-875-233-4 |
| 7 | 14 | 100.0 | 218 | 3 | US-08-875-233-6 |
| 8 | 14 | 100.0 | 218 | 3 | US-08-875-233-15 |
| 9 | 14 | 100.0 | 218 | 3 | US-09-127-742-2 |
| 10 | 14 | 100.0 | 218 | 3 | US-09-127-742-4 |
| 11 | 14 | 100.0 | 218 | 6 | 5422259-4 |
| 12 | 12 | 85.7 | 218 | 6 | 5422259-4 |
| 13 | 6 | 42.9 | 82 | 4 | US-08-875-233-10 |
| 14 | 6 | 42.9 | 116 | 4 | US-09-513-999C-7876 |
| 15 | 6 | 42.9 | 146 | 4 | US-09-252-991A-24703 |
| 16 | 6 | 42.9 | 203 | 4 | US-09-252-991A-22678 |
| 17 | 6 | 42.9 | 246 | 4 | US-09-252-991A-30450 |
| 18 | 6 | 42.9 | 258 | 4 | US-09-252-991A-22452 |
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| 23 | 6 | 42.9 | 373 | 4 | US-09-252-991A-24381 |
| 24 | 6 | 42.9 | 462 | 4 | US-09-252-991A-18187 |
| 25 | 6 | 42.9 | 516 | 4 | US-09-252-991A-17933 |
| 26 | 6 | 42.9 | 521 | 4 | US-09-252-991A-25791 |
| 27 | 6 | 42.9 | 532 | 4 | US-09-248-796A-19478 |

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|----|---|------|------|---|----------------------|--------------------|
| 28 | 6 | 42.9 | 561 | 4 | US-09-812-079A-2 | Sequence 2, Appli |
| 29 | 6 | 42.9 | 576 | 4 | US-09-252-991A-23246 | Sequence 23246, A |
| 30 | 6 | 42.9 | 579 | 4 | US-09-171-699-6 | Sequence 6, Appli |
| 31 | 6 | 42.9 | 579 | 4 | US-09-171-699-8 | Sequence 8, Appli |
| 32 | 6 | 42.9 | 631 | 1 | US-08-605-541B-12 | Sequence 12, Appli |
| 33 | 6 | 42.9 | 642 | 4 | US-09-248-796A-19191 | Sequence 19191, A |
| 34 | 6 | 42.9 | 663 | 4 | US-09-194-468A-30 | Sequence 30, Appli |
| 35 | 6 | 42.9 | 735 | 4 | US-09-252-991A-18657 | Sequence 18657, A |
| 36 | 6 | 42.9 | 1011 | 4 | US-09-252-991A-32419 | Sequence 32419, A |
| 37 | 6 | 42.9 | 1466 | 4 | US-09-252-991A-30085 | Sequence 30085, A |
| 38 | 6 | 42.9 | 2137 | 3 | US-09-134-001C-4463 | Sequence 4463, Ap |
| 39 | 5 | 35.7 | 9 | 1 | US-08-615-181-93 | Sequence 93, Appli |
| 40 | 5 | 35.7 | 10 | 1 | US-08-090-193-36 | Sequence 36, Appli |
| 41 | 5 | 35.7 | 10 | 2 | US-08-488-031-36 | Sequence 36, Appli |
| 42 | 5 | 35.7 | 10 | 2 | US-08-486-569-36 | Sequence 36, Appli |
| 43 | 5 | 35.7 | 10 | 2 | US-08-488-027-36 | Sequence 36, Appli |
| 44 | 5 | 35.7 | 10 | 2 | US-08-090-192-36 | Sequence 36, Appli |
| 45 | 5 | 35.7 | 10 | 2 | US-08-482-663-36 | Sequence 36, Appli |

ALIGNMENTS

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RESULT 1
5422259-2
; Patent No. 5422259
; APPLICANT: DE BOTH, MICHEL, BEN TAHAR, SOPHIA, NOEL, MARIANNE;
; PERRET, JOEL
; TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE
; SPECIES CUCUMIS MELO
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/27,563
; FILING DATE: 05-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,255
; FILING DATE: 13-AUG-1990
; SEQ ID NO:2:
; LENGTH: 217
5422259-2

Query Match          100.0%; Score 14; DB 6; Length 217;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ox      1 MDKSESTSGRNR 14
Db      1 MDKSESTSGRNR 14

RESULT 2
US-08-398-209-2
; Sequence 2, Application US/08398209
; Patent No. 5789656
; GENERAL INFORMATION:
; APPLICANT: Deboth, Michiel
; APPLICANT: No. 57896561, Marianne
; APPLICANT: Ben Tahar, Sophia
; TITLE OF INVENTION: Transgenic Plants Belonging to the
; SPECIES CUCUMIS MELO
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5789656west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,209
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,563
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/566,255
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 8910848
FILING DATE: 11-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A.
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.21US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-398-209-2

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
DB 1 MDKSESTSAGRNR 14

RESULT 3
US-08-398-209-4
Sequence 4, Application US/08398209
Patent No. 5789656
GENERAL INFORMATION:
APPLICANT: DeBoch, Michael
APPLICANT: No. 57896561, Marianne
APPLICANT: Ben Tahar, Sophia
APPLICANT: Perret, Joel
TITLE OF INVENTION: Transgenic Plants Belonging to the
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5789656west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,209
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,563
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/566,255
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 8910848
FILING DATE: 11-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A.
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.21US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-398-209-4

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
DB 1 MDKSESTSAGRNR 14

RESULT 4
US-08-553-619B-3
Sequence 3, Application US/08553619B
Patent No. 5819705
GENERAL INFORMATION:
APPLICANT: Dehaan, Petrus T.
TITLE OF INVENTION: Virus Resistant Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5819705artis Crop Protection
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,619B
FILING DATE: December 1, 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 137-1082/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/354-3588
TELEFAX: 415/857-1125
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-619B-3

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
DB 1 MDKSESTSAGRNR 14

RESULT 5
US-08-875-233-2
Sequence 2, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-2

Query Match 100.0%; Score 14; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 6
US-08-875-233-4
Sequence 4, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-4

Query Match 100.0%; Score 14; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSAGRNR 14
Db 1 MDKSESTSAGRNR 14

RESULT 7
US-08-875-233-6
Sequence 6, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-6

Query Match 100.0%; Score 14; DB 3; Length 218;

Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGRNR 14
|||||
DB 1 MDKSESTSGRNR 14

RESULT 8

US-08-875-233-15
Sequence 15, Application US/08875233
Patent No. 6127601

GENERAL INFORMATION:
APPLICANT: Boeshore, Maury L.
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M.
APPLICANT: Reynolds, John F.
APPLICANT: Carney, Kim J.
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rocket, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Scetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60089
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-15

Query Match 100.0%; Score 14; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGRNR 14
|||||
DB 1 MDKSESTSGRNR 14

RESULT 9

US-09-127-742-2
Sequence 2, Application US/09127742A
Patent No. 6198022

GENERAL INFORMATION:
APPLICANT: DE BOTH, MICHAEL
APPLICANT: NOEL, MARIANNE
APPLICANT: TAHAR, SOPHIA BEN
APPLICANT: PERRET, JOEL
APPLICANT: BIOSEM
TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE SPECIES CUCUMIS MELO
FILE REFERENCE: 8076.21USD2
CURRENT APPLICATION NUMBER: US/09/127,742A
CURRENT FILING DATE: 1998-08-03

EARLIER APPLICATION NUMBER: 08/398,209
EARLIER FILING DATE: 1995-03-02
EARLIER APPLICATION NUMBER: 08/027,563
EARLIER FILING DATE: 1993-03-05
EARLIER APPLICATION NUMBER: 07/566,255
EARLIER FILING DATE: 1990-08-13
EARLIER APPLICATION NUMBER: FR 89 10848
EARLIER FILING DATE: 1989-08-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 218
TYPE: PRT
ORGANISM: cucumber mosaic virus
US-09-127-742-2

Query Match 100.0%; Score 14; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGRNR 14
|||||
DB 1 MDKSESTSGRNR 14

RESULT 10

US-09-127-742-4
Sequence 4, Application US/09127742A
Patent No. 6198022
GENERAL INFORMATION:
APPLICANT: DE BOTH, MICHAEL
APPLICANT: NOEL, MARIANNE
APPLICANT: TAHAR, SOPHIA BEN
APPLICANT: PERRET, JOEL
APPLICANT: BIOSEM
TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE SPECIES CUCUMIS MELO
FILE REFERENCE: 8076.21USD2
CURRENT APPLICATION NUMBER: US/09/127,742A
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: 08/398,209
EARLIER FILING DATE: 1995-03-02
EARLIER APPLICATION NUMBER: 08/027,563
EARLIER FILING DATE: 1993-03-05
EARLIER APPLICATION NUMBER: 07/566,255
EARLIER FILING DATE: 1990-08-13
EARLIER APPLICATION NUMBER: FR 89 10848
EARLIER FILING DATE: 1989-08-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 218
TYPE: PRT
ORGANISM: cucumber mosaic virus
US-09-127-742-4

Query Match 100.0%; Score 14; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGRNR 14
|||||
DB 1 MDKSESTSGRNR 14

RESULT 11

US-09-127-742-2
Sequence 2, Application US/09127742A
Patent No. 6198022
GENERAL INFORMATION:
APPLICANT: DE BOTH, MICHAEL
APPLICANT: NOEL, MARIANNE
APPLICANT: TAHAR, SOPHIA BEN
APPLICANT: PERRET, JOEL
APPLICANT: BIOSEM
TITLE OF INVENTION: TRANSGENIC PLANTS BELONGING TO THE SPECIES CUCUMIS MELO
FILE REFERENCE: 8076.21USD2
CURRENT APPLICATION NUMBER: US/09/127,742A
CURRENT FILING DATE: 1998-08-03

APPLICATION NUMBER: US/08/27,563
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 566,255
FILING DATE: 13-AUG-1990
SEQ ID NO: 4
LENGTH: 218
5422259-4

Query Match 100.0%; Score 14; DB 6; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGRRR 14
Db 1 MDKSESTSGRRR 14

RESULT 12
US-08-875-233-10
Sequence 10, Application US/08875233
Patent No. 6127601
GENERAL INFORMATION:

APPLICANT: Boeshore, Maury L
APPLICANT: McMaster, J. Russell
APPLICANT: Tricoli, David M
APPLICANT: Reynolds, John F
APPLICANT: Carney, Kim J
TITLE OF INVENTION: Plants Resistant to C Strains of
TITLE OF INVENTION: Cucumber Mosaic Virus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Rocket, Milnamow & Katz, Ltd.
STREET: 2 Prudential Plaza, 180 N. Steetson, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60689

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,233
FILING DATE: 26-JUN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lisa V. Mueller
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-233-10

Query Match 85.7%; Score 12; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTSGRRN 12
Db 1 MDKSESTSGRRN 12

RESULT 13
US-09-252-991A-22748
Sequence 22748, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22748

LENGTH: 82
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22748

Query Match 42.9%; Score 6; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AGRNR 14
Db 36 AGRNR 41

RESULT 14
US-09-513-999C-7876
Sequence 7876, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.ppt
SEQ ID NO 7876
LENGTH: 116
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -19...-1
OTHER INFORMATION: score 5.8
OTHER INFORMATION: seq H1MS1VTSASA/SA
FEATURE:
NAME/KEY: UNSURE
LOCATION: 62
OTHER INFORMATION: Xaa= * or Cys or Trp
FEATURE:
NAME/KEY: UNSURE
LOCATION: 79
OTHER INFORMATION: Xaa=Leu or Trp
FEATURE:
NAME/KEY: UNSURE
LOCATION: 81
OTHER INFORMATION: Xaa=Arg or Ser
US-09-513-999C-7876

Query Match 42.9%; Score 6; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TSAGRN 12
Db 7 TSAGRN 12

Db 63 TSAGRN 68

RESULT 15

US-09-252-991A-24703
 ; Sequence 24703, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24703
 ; LENGTH: 146
 ; TYPE: PR1
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24703

Query Match 42.9%; Score 6; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 AGRNR 14
 |||||
 Db 131 AGRNR 136

Search completed: December 5, 2004, 08:17:48
 Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 5, 2004, 08:07:32 ; Search time 21 Seconds
(without alignments)
64.145 Million cell updates/sec

Title: US-09-857-841-4
Perfect score: 14
Sequence: 1 MDKSESTSGAGNRR 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|----------------------|
| 1 | 14 | 100.0 | 218 | 1 JQ1253 | coat protein - cuc |
| 2 | 14 | 100.0 | 218 | 1 JQ1254 | coat protein - cuc |
| 3 | 14 | 100.0 | 218 | 1 JS0090 | coat protein - cuc |
| 4 | 14 | 100.0 | 218 | 1 JCVXY1 | coat protein - cuc |
| 5 | 14 | 100.0 | 218 | 2 JCG075 | coat protein - cuc |
| 6 | 14 | 100.0 | 218 | 2 S42098 | coat protein - cuc |
| 7 | 14 | 100.0 | 218 | 2 S58039 | capsid protein - cuc |
| 8 | 14 | 100.0 | 218 | 2 JCG074 | coat protein - cuc |
| 9 | 14 | 100.0 | 218 | 2 JCG073 | coat protein - cuc |
| 10 | 14 | 100.0 | 218 | 2 S09663 | coat protein - cuc |
| 11 | 12 | 85.7 | 218 | 1 JAO135 | coat protein - cuc |
| 12 | 12 | 50.0 | 218 | 2 D71392 | coat protein - cuc |
| 13 | 6 | 42.9 | 108 | 2 UQ2176 | hypothetical 11.5K |
| 14 | 6 | 42.9 | 133 | 2 T17609 | hypothetical prote |
| 15 | 6 | 42.9 | 133 | 2 T47771 | hypothetical prote |
| 16 | 6 | 42.9 | 163 | 2 JQ0139 | hypothetical 17.8K |
| 17 | 6 | 42.9 | 174 | 2 S28733 | hypothetical prote |
| 18 | 6 | 42.9 | 202 | 2 T08230 | hypothetical prote |
| 19 | 6 | 42.9 | 226 | 2 T24125 | hypothetical prote |
| 20 | 6 | 42.9 | 228 | 2 E83109 | hypothetical prote |
| 21 | 6 | 42.9 | 264 | 2 T39141 | transcription fact |
| 22 | 6 | 42.9 | 268 | 2 T24118 | hypothetical prote |
| 23 | 6 | 42.9 | 270 | 2 T24126 | hypothetical prote |
| 24 | 6 | 42.9 | 351 | 2 E87451 | conserved hypotet |
| 25 | 6 | 42.9 | 436 | 2 T00756 | hypothetical prote |
| 26 | 6 | 42.9 | 445 | 2 E84714 | probable protein k |
| 27 | 6 | 42.9 | 449 | 2 E97428 | chemotaxis motD pr |
| 28 | 6 | 42.9 | 449 | 2 AF2646 | chemotaxis MotD pr |
| 29 | 6 | 42.9 | 496 | 2 T34760 | oligopeptide ABC t |

| | | | | | |
|----|---|------|------|----------|---------------------|
| 30 | 6 | 42.9 | 497 | 2 T33634 | hypothetical prote |
| 31 | 6 | 42.9 | 561 | 1 WMBETW | 65K lower matrix p |
| 32 | 6 | 42.9 | 561 | 1 WMBE65 | 65K lower matrix p |
| 33 | 6 | 42.9 | 662 | 2 A42496 | gelatinase A (EC 3 |
| 34 | 6 | 42.9 | 662 | 2 S34780 | gelatinase A (EC 3 |
| 35 | 6 | 42.9 | 663 | 1 S46492 | gelatinase A (EC 3 |
| 36 | 6 | 42.9 | 742 | 2 H95270 | probable kinase/es |
| 37 | 6 | 42.9 | 1006 | 2 T13331 | probable tail prote |
| 38 | 6 | 42.9 | 1143 | 2 T28129 | hypothetical prote |
| 39 | 6 | 42.9 | 1275 | 2 T33369 | hypothetical prote |
| 40 | 6 | 42.9 | 1750 | 2 E86151 | hypothetical prote |
| 41 | 6 | 42.9 | 2160 | 2 T20241 | hypothetical prote |
| 42 | 6 | 42.9 | 2570 | 2 T17451 | limbriac-associate |
| 43 | 6 | 42.9 | 2693 | 2 A40743 | IP3 receptor, XIP3 |
| 44 | 6 | 42.9 | 3562 | 2 A47171 | chondroitin sulfat |
| 45 | 5 | 35.7 | 26 | 2 S04376 | hypothetical prote |

ALIGNMENTS

RESULT 1
JQ1253
C:Species: cucumber mosaic virus (strain FC)
C:Date: 31-Mar-1992 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C:Accession: JQ1253
R:Shintaku, M.
U. Gen. Virol. 72, 2587-2589, 1991
A:Title: Coat protein gene sequences of two cucumber mosaic virus strains reveal a single
A:Reference number: JQ1253; MUID:92013983; PMID:1919534
A:Accession: JQ1253
A:Molecule type: genomic RNA
A:Residues: 1-218 <SHI>
A:Cross-references: UNIPROT:Q00259; GB:D10544; NID:g222024; PID:BA01403.1; PID:g222025
A:Note: Comparison of the amino acid sequence of this protein to that of strain P6 shows
R:Tsunaawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A:Title: Micro-identification of amino-terminal acetyl amino acids in proteins.
A:Reference number: A61297; MUID:83056735; PMID:6754709
A:Contents: annotation; acetylation
C:Comment: This cucumber mosaic virus strain induces a yellow chlorosis.
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDKSESTSGAGNRR 14
Db 1 MDKSESTSGAGNRR 14

RESULT 2
JQ1254
C:Species: cucumber mosaic virus (strain P6)
C:Date: 31-Mar-1992 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C:Accession: JQ1254
R:Shintaku, M.
U. Gen. Virol. 72, 2587-2589, 1991
A:Title: Coat protein gene sequences of two cucumber mosaic virus strains reveal a single
A:Reference number: JQ1253; MUID:92013983; PMID:1919534
A:Accession: JQ1254
A:Molecule type: genomic RNA
A:Residues: 1-218 <SHI>
A:Cross-references: UNIPROT:Q00261; GB:D10545; NID:g222026; PID:BA01404.1; PID:g222027
A:Note: Comparison of the amino acid sequence of this protein to that of strain FC shows
R:Tsunaawa, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A:Title: Micro-identification of amino-terminal acetyl amino acids in proteins.

A:Reference number: A61297; MUID:83056735; PMID:6754709
A:Contents: annotation; acetylation
C:Comment: This cucumber mosaic virus strain induces a yellow chlorosis.
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
|||
Db 1 MDKSESTSGRNR 14

RESULT 3
US0090
coat protein - cucumber mosaic virus (strain O)
C:Species: cucumber mosaic virus, CMV
C:Date: 31-Mar-1992 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C:Accession: J06090; PS0314
R:Hayakawa, T.; Mizukami, M.; Nakajima, M.; Suzuki, M.
U: Gen. Virol. 70, 499-504, 1989
A:Title: Complete nucleotide sequence of RNA 3 from cucumber mosaic virus (CMV) strain C
A:Reference number: J06089; MUID:89279231; PMID:2732698
A:Accession: J06090
A:Molecule type: mRNA
A:Residues: 1-218 <HAY>
A:Cross-references: UNIPROT:P16489; GB:D00385; NID:9222030; PID:BA00297.1; PID:9222032
A:Accession: PS0314
A:Molecule type: protein
A:Residues: 216-218 <HA2>
R:Tsunasawa, S.; Narita, K.
U: Biochem. 92, 607-613, 1982
A:Title: Micro-identification of amino-terminal acetylamino acids in proteins.
A:Reference number: A61297; MUID:83056735; PMID:6754709
A:Contents: annotation; acetylation
C:Genetics:
A:Map position: segment 3
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
|||
Db 1 MDKSESTSGRNR 14

RESULT 4
VCVX1
coat protein - cucumber mosaic virus (strain Y)
C:Species: cucumber mosaic virus, CMV
A:Note: host Nicotiana tabacum cv. Xanthi nc (tobacco)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: J00957
R:Nitta, N.; Masuta, C.; Kuwata, S.; Takamaki, Y.
Ann. Phytopathol. Soc. Jpn. 54, 516-522, 1989
A:Title: Comparative studies on the nucleotide sequence of cucumber mosaic virus RNA3 de
A:Reference number: J00956
A:Accession: J00957
A:Molecule type: mRNA
A:Residues: 1-218 <NIT>
A:Cross-references: UNIPROT:P18027
R:Tsunasawa, S.; Narita, K.
U: Biochem. 92, 607-613, 1982
A:Title: Micro-identification of amino-terminal acetylamino acids in proteins.
A:Reference number: A61297; MUID:83056735; PMID:6754709
A:Contents: annotation; acetylation

C:Comment: The genome consists of three single-stranded, positive RNAs, designated RNA1,
C:Genetics:
A:Map position: segment RNA3
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 14; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
|||
Db 1 MDKSESTSGRNR 14

RESULT 5
JC6075
coat protein - cucumber mosaic virus (strain CS)
C:Species: cucumber mosaic virus, CMV
C:Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C:Accession: JC6075
R:Huang, L.; Hu, J.S.; Barry, K.; Hweichung, F.
Chinese J. Virol. 12, 235-242, 1996
A:Title: Coat protein gene sequence analysis of three cucumber mosaic virus strains infec
A:Reference number: JC6073
A:Accession: JC6075
A:Molecule type: mRNA
A:Residues: 1-218 <HUA>
A:Cross-references: UNIPROT:Q8JPK2; UNIPROT:Q9DXJ2; UNIPROT:Q9LPE5; UNIPROT:Q9DXJ3; UNIP
ROT:Q8JPK0; UNIPROT:Q9JW5; UNIPROT:Q9LPP6; UNIPROT:Q9JFY4; UNIPROT:Q8JPK4; UNIPROT:Q9D
6132; UNIPROT:Q9YJ52; UNIPROT:Q8JPK8; UNIPROT:Q9EN66; UNIPROT:Q8J259; UNIPROT:Q9DWM2; UN
A:Experimental source: strain CS
A:Note: the authors translated the codon CCG for residue 83 as Gly
C:Genetics:
A:Gene: cp
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: coat protein

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
|||
Db 1 MDKSESTSGRNR 14

RESULT 6
S42098
coat protein - cucumber mosaic virus
C:Species: cucumber mosaic virus, CMV
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S42098
R:Hyon, S.; Park, Y.I.
submitted to the EMBL Data Library, February 1994
A:Description: Nucleotide sequence of cDNA from RNA4 of cucumber mosaic virus-A8 the Kor
A:Reference number: S42098
A:Accession: S42098
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-218 <HYO>
A:Cross-references: UNIPROT:Q66154; EMBL:X77855; NID:9457166; PID:CAA54846.1; PID:945716
C:Superfamily: cucumber mosaic virus coat protein

Query Match 100.0%; Score 14; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKSESTSGRNR 14
|||
Db 1 MDKSESTSGRNR 14


```
RESULT 7
S58039
capaid protein - cucumber mosaic virus
C/Species: cucumber mosaic virus, CMV
C/Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S58039
R/Haq, O.M.R.
submitted to the EMBL Data Library, July 1995
A/Reference number: S58039
A/Accession: S58039
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-218 <HAQ>
A/Cross-references: UNIPROT:Q66157; EMBL:X89652; NID:g902619; PIDN:CAA61802.1; PID:g9026
C:Superfamily: cucumber mosaic virus coat protein

Query Match
Best Local Similarity 100.0%; Score 14; DB 2; Length 218;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy
1 MDKSESTSGAGNRR 14
|||||
1 MDKSESTSGAGNRR 14

RESULT 8
JC6074
coat protein - cucumber mosaic virus (strain MM)
C/Species: cucumber mosaic virus, CMV
C/Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C/Accession: JC6074
R/Huaping, L.; Hu, J.S.; Barry, K.; Hweichung, F.
Chinese J. Virol. 12, 235-242, 1996
A/Title: Coat protein gene sequence analysis of three cucumber mosaic virus strains infe
A/Reference number: JC6073
A/Accession: JC6074
A/Molecule type: mRNA
A/Residues: 1-218 <HNA>
A/Cross-references: UNIPROT:Q83257; UNIPROT:O55251; UNIPROT:Q9WAB3; UNIPROT:Q9YJR9; UNIF
A/Experimental source: strain MM
A/Note: the authors translated the codon CGT for residue 30 as Ala
C/Genetics:
A/Genes: cp
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: coat protein

Query Match
Best Local Similarity 100.0%; Score 14; DB 2; Length 218;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy
1 MDKSESTSGAGNRR 14
|||||
1 MDKSESTSGAGNRR 14

RESULT 9
JC6073
coat protein - cucumber mosaic virus (strain BS)
C/Species: cucumber mosaic virus, CMV
C/Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C/Accession: JC6073
R/Huaping, L.; Hu, J.S.; Barry, K.; Hweichung, F.
Chinese J. Virol. 12, 235-242, 1996
A/Title: Coat protein gene sequence analysis of three cucumber mosaic virus strains infe
A/Reference number: JC6073
A/Accession: JC6073
A/Molecule type: mRNA
A/Residues: 1-218 <HNA>
A/Cross-references: UNIPROT:Q9DUW8; UNIPROT:Q9YJR7; UNIPROT:Q8JPK1; UNIPROT:Q9E2V6; UNIF
PROT:Q91PP6; UNIPROT:Q9JFY4; UNIPROT:Q66157; UNIPROT:Q66130; UNIPROT:Q8JPK4; UNIPROT:Q9J
6132; UNIPROT:Q9YJS2; UNIPROT:Q8JPM8; UNIPROT:Q9ENSE6; UNIPROT:Q83259; UNIPROT:Q9DWM2; UN
A/Experimental source: strain BS
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A/Note: the authors translated the codon CCA for residue 56 as Thr and CCC for residue 5;
C/Genetics:
A/Genes: cp
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: coat protein

Query Match
Best Local Similarity 100.0%; Score 14; DB 2; Length 218;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy
1 MDKSESTSGAGNRR 14
|||||
1 MDKSESTSGAGNRR 14

RESULT 10
S09663
coat protein - cucumber mosaic virus (strain I17F)
C/Species: cucumber mosaic virus, CMV
A/Variety: strain I17F
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S09663; S06932
R/Noel, M.J.T.; Tahar, S.B.
Nucleic Acids Res. 18, 1332, 1990
A/Title: Corrigendum. Nucleotide sequence of the coat protein gene and flanking regions
A/Reference number: S09663; MUID:90206832; PMID:2320436
A/Accession: S09663
A/Molecule type: mRNA
A/Residues: 1-218 <NOE>
A/Cross-references: UNIPROT:P14767
A/Experimental source: strain I17F
A/Note: this is a revision to the sequence from reference S06932
R/Noel, M.J.T.; Tahar, S.B.
Nucleic Acids Res. 17, 10492, 1989
A/Title: Nucleotide sequence of the coat protein gene and flanking regions of Cucumber M
A/Reference number: S06932; MUID:90098885; PMID:2602158
A/Accession: S06932
A/Molecule type: mRNA
A/Residues: 1-6,'W','8','44','W','46-51','W','53-56','W','58-68','W','70','W','72-73','W','75-96','W','98-
A/Cross-references: EMBL:X16386
A/Experimental source: strain I17F
A/Note: this sequence has been revised in reference S09663
C:Superfamily: cucumber mosaic virus coat protein

Query Match
Best Local Similarity 100.0%; Score 14; DB 2; Length 218;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy
1 MDKSESTSGAGNRR 14
|||||
1 MDKSESTSGAGNRR 14

RESULT 11
JA0136
coat protein - cucumber mosaic virus (strain C)
C/Species: cucumber mosaic virus, CMV
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: JA0136
R/Quemada, H.; Kearney, C.; Gonsalves, D.; Slightom, J.L.
J. Gen. Virol. 70, 1065-1073, 1989
A/Title: Nucleotide sequences of the coat protein genes and flanking regions of cucumber
A/Reference number: JU0087; MUID:89279284; PMID:2732712
A/Accession: JA0136
A/Cross-references: UNIPROT:P21368; GB:D00462; NID:g222041; PIDN:BAA00357.1; PID:g222042
A/Residues: 1-218 <QBE>
A/Molecule type: genomic RNA
A/Genes: CP
R/Tsunawake, S.; Narita, K.
J. Biochem. 92, 607-613, 1982
A/Title: Micro-identification of amino-terminal acetyl amino acids in proteins.
A/Reference number: A61297; MUID:83056735; PMID:6754709
A/Contents: annotation; acetylation
C/Genetics:
```

A:Map position: segment RNA3
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein; glycoprotein
F:1/Modified site: acetylated amino end (Met) #status experimental
F:43/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.7%; Score 12; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKSESTISAGRN 12
Db 1 MDKSESTISAGRN 12

RESULT 12
D71392
coat protein - cucumber mosaic virus (strain Ixora)
N:Alternate names: capsid protein
C:Species: cucumber mosaic virus, CMV
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C:Accession: D71392
R:McGarry, P.; Tounisiant, M.; Geletcka, L.; Cellini, F.; Kaper, J.M.
J. Gen. Virol. 76, 2257-2270, 1995
A:Title: The complete sequence of a cucumber mosaic virus from Ixora that is deficient 1
A:Reference number: A71392; MUID:96005047; PMID:7561763
A:Accession: D71392
A:Molecule type: mRNA
A:Residues: 1-218 <MG>
A:Cross-references: UNIPROT:Q66120; GB:U20219; NID:G161916; PIDN:AMC54619.1; PID:G11619
A:Experimental source: strain Ixora
C:Comment: The CMV genome consists of three species of single-stranded, capped, positive
C:Comment: The Ixora strain is unusual in that it does not replicate several well charac
ptoms found when replicated by other CMV strains.
C:Genetics:
A:Map position: segment RNA 3
C:Superfamily: cucumber mosaic virus coat protein
C:Keywords: acetylated amino end; coat protein
F:1/Modified site: acetylated amino end (Met) #status predicted

Query Match 50.0%; Score 7; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 SAGRNRR 14
Db 8 SAGRNRR 14

RESULT 13
JQ2176
hypothetical 11.5K protein (clone GV-B) - garlic virus B
N:Alternate names: hypothetical protein II
C:Species: garlic virus B
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: JQ2176; S27912
R:Sumi, S.; Tsuneyoshi, T.; Furutani, H.
J. Gen. Virol. 74, 1879-1885, 1993
A:Title: Novel rod-shaped viruses isolated from garlic, Allium sativum, possessing a uni
A:Reference number: JQ2171; MUID:93389442; PMID:8376963
A:Accession: JQ2176
A:Molecule type: mRNA
A:Residues: 1-108 <SUM>
A:Cross-references: UNIPROT:Q67695; GB:AB010301; GB:D11158; NID:G2826152; PIDN:BAA61814.
R:Sumi, S.T.
submitted to the EMBL Data Library, July 1992
A:Reference number: S27908
A:Accession: S27912
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <SUM>
A:Cross-references: EMBL:D11158; NID:G221432; PIDN:BAA61814.1; PID:G221433
C:Superfamily: barley stripe mosaic virus 14K protein

Query Match 42.9%; Score 6; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SESTSA 9
Db 100 SESTSA 105

RESULT 14
T17609
hypothetical protein a119L - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17609
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: T17609
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-133 <GRA>
A:Cross-references: UNIPROT:Q84440; EMBL:U42580; NID:G4028896; PIDN:AMC96487.1
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A:Note: a119L

Query Match 42.9%; Score 6; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 STSAGR 11
Db 128 STSAGR 133

RESULT 15
T47771
hypothetical protein F2413.190 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47771
R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Stert, W.; Holland, R.; Welchseigartner, M.;
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24475
A:Accession: T47771
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <NYA>
A:Cross-references: UNIPROT:Q9M119; EMBL:AL138655
A:Experimental source: cultivar Columbia; BAC clone F2413
C:Genetics:
A:Map position: 3
A:Note: F2413.190
C:Superfamily: Arabidopsis thaliana hypothetical protein F2413.190

Query Match 42.9%; Score 6; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SESTSA 9
Db 6 SESTSA 11

Search completed: December 5, 2004, 08:17:19
Job time : 22 secs